

QY 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSVSWIKGDSPLRENSRIALVESGLRIHNV 180
 Db 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSVSWIKGDSPLRENSRIALVESGLRIHNV 180
 QY 181 OKEDAGGYRCYAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
 Db 181 OKEDAGGYRCYAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
 QY 241 PTTWIENGNAVSSGSIOESYKDRVIDSRLOLFTTKRGLYCIATNKGKEFSTAKKAAT 300
 Db 241 PTTWIENGNAVSSGSIOESYKDRVIDSRLOLFTTKRGLYCIATNKGKEFSTAKKAAT 300
 QY 301 ISIAEMSKPDKNKGCAQYAGVEVCNAVL-----AKDALVEL-NTSYADPEADQELLVHT 354
 Db 301 ISIAEMSKPDKNKGCAQYAGVEVCNAVL-----AKDALVEL-NTSYADPEADQELLVHT 354
 QY 354 AMNELKAVSPVCPRAEALLCNHIFQECSPGVPTPIPCREYCLAVKELFCAKEMWYME 414
 Db 354 AMNELKAVSPVCPRAEALLCNHIFQECSPGVPTPIPCREYCLAVKELFCAKEMWYME 414
 Y 415 EKHRLGLYRSEMHLLSVKCSKLPMSHMDPTACARLPDLVKNKELKTFPPMTSSKPSVD 474
 Db 415 EKHRLGLYRSEMHLLSVKCSKLPMSHMDPTACARLPDLVKNKELKTFPPMTSSKPSVD 474
 QY 475 IPNLPSSSSSSFSPYPTSMVTIISIMSSFAIFVLLITTTLYCCRRRKKOMKKRESAY 534
 Db 475 IPNLPSSSSSSFSPYPTSMVTIISIMSSFAIFVLLITTTLYCCRRRKKOMKKRESAY 534
 QY 535 TLTTLPSSELLDRLPNMYQRMPLLNPKLISLEYPRNNIEYVADIGEAGFRYFOARA 594
 Db 535 TLTTLPSSELLDRLPNMYQRMPLLNPKLISLEYPRNNIEYVADIGEAGFRYFOARA 594
 QY 595 PGLLPYEPFTVAAYKMLEEASADMQADFOREALMAEFNDPNYIKLGVCAVCGPKMLL 654
 Db 595 PGLLPYEPFTVAAYKMLEEASADMQADFOREALMAEFNDPNYIKLGVCAVCGPKMLL 654
 QY 655 FEYMAVGDNLNFIKSMSPHTVCSLSHSDLSMPRAQVSSGPPPLSCAEQLCIARQVAAAMA 714
 Db 655 FEYMAVGDNLNFIKSMSPHTVCSLSHSDLSMPRAQVSSGPPPLSCAEQLCIARQVAAAMA 714
 QY 715 YLSEKKEFPHRLDTRNCLVGENMYVKIADPGLSRNITYSADYKKNENAIPIRMMPPSI 774
 Db 715 YLSEKKEFPHRLDTRNCLVGENMYVKIADPGLSRNITYSADYKKNENAIPIRMMPPSI 774
 QY 775 FYNRTTESDWAYGVVLMEIFSYGLQPYGYGMAHEVITYYVRDGNILSCPENCPVELYNL 834
 Db 775 FYNRTTESDWAYGVVLMEIFSYGLQPYGYGMAHEVITYYVRDGNILSCPENCPVELYNL 834
 QY 835 MRLCWSKLPADRPSTSTHRIILERMKCEBAEGTASY 869
 Db 835 MRLCWSKLPADRPSTSTHRIILERMKCEBAEGTASY 869
 Db 837 MRLCWSKLPADRPSTSTHRIILERMKCEBAEGTASY 871

RESULT 2
 148697 protein-tyrosine kinase (EC 2.7.1.112) nsk2 precursor, splice form 1 - mouse
 N:Alternate names: receptor-type tyrosine kinase
 C:Contains: protein-tyrosine kinase nsk2 precursor, splice form 3
 C:Species: Mus musculus (house mouse)
 C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
 C:Accession: 148697; S60740
 R:Ganju, P.; Walls, E.; Brennan, J.; Relth, A.D.
 A:Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase
 A:Reference number: 148696; MUID:95349951
 A:Accession: 148697
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-881 <GAN1>
 A:Cross-references: EMBL:X86445; NID:g929725; PID:CA60166.1; PID:g929726
 A:Experimental source: splice form 1
 A:Accession: S60740

A:Molecule type: DNA
 A:Residues: 1-456, 'A', 466-881 <GAN2>
 A:Cross-references: EMBL:X86445; NID:g929725
 A:Experimental source: splice form 3
 C:Comment: For alternate splice forms see PIR:148696.
 C:Genetics:
 A:Gene: nsk2
 A:Cross-references: MGI:103308
 C:Superfamily: mouse ror-related receptor; immunoglobulin homology; protein kinase ho
 C:Keywords: ATP; glycoprotein; phosphotransferase; receptor; transmembrane protein; t
 F:1-21/Domain: signal sequence #status predicted <Sig>
 F:22-881/Product: protein-tyrosine kinase nsk2, splice form 1 #status predicted <Mat1
 F:22-456, 'A', 466-881/Product: protein-tyrosine kinase nsk2, splice form 3 #status pre
 F:42-101/Domain: immunoglobulin homology <IM1>
 F:135-192/Domain: immunoglobulin homology <IM2>
 F:226-284/Domain: immunoglobulin homology <IM3>
 F:498-518/Domain: transmembrane #status predicted <TRM>
 F:575-865/Domain: protein kinase homology <Kin>
 F:583-591/Region: protein kinase ATP-binding motif
 F:222,462/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.3% Score 4128; DB 1; Length 881;
 Best Local Similarity 90.4% Pred. No. 1,9e-199;
 Matches 788; Conservative 30; Mismatches 44; Indels 10; Gaps 4;

QY 1 MRELVINPLVHLLTVAESGTEKLPKAVITPTLETVDALVEVATEKCAVESYPOPEIS 60
 Db 1 MRELVINPLQMLTLVARSSTGTEKLPKPVVATPLETVDALVEVATEKCAVESYPOPEIS 60
 QY 61 WTRNKILIKLDPTRKSTIENQQLTILSVESDQGYICCTANNVGAVESGALQVYMK 120
 Db 61 WTRNKILIKLDPTRKSTIENQQLTILSVESDQGYICCTANNVGAVESGALQVYMK 120
 QY 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSVSWIKGDSPLRENSRIALVESGLRIHNV 180
 Db 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSVSWIKGDSPLRENSRIALVESGLRIHNV 180
 QY 181 OKEDAGGYRCYAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
 Db 181 OKEDAGGYRCYAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
 QY 241 PTTWIENGNAVSSGSIOESYKDRVIDSRLOLFTTKRGLYCIATNKGKEFSTAKKAAT 300
 Db 241 PTTWIENGNAVSSGSIOESYKDRVIDSRLOLFTTKRGLYCIATNKGKEFSTAKKAAT 300
 QY 301 ISIAEMSKPDKNKGCAQYAGVEVCNAVL-----AKDALVEL-NTSYADPEADQELLVHT 354
 Db 301 ISIAEMSKPDKNKGCAQYAGVEVCNAVL-----AKDALVEL-NTSYADPEADQELLVHT 354
 QY 354 AMNELKAVSPVCPRAEALLCNHIFQECSPGVPTPIPCREYCLAVKELFCAKEMWYME 414
 Db 354 AMNELKAVSPVCPRAEALLCNHIFQECSPGVPTPIPCREYCLAVKELFCAKEMWYME 414
 QY 415 EKHRLGLYRSEMHLLSVKCSKLPMSHMDPTACARLPDLVKNKELKTFPPMTSSKPSVD 474
 Db 415 EKHRLGLYRSEMHLLSVKCSKLPMSHMDPTACARLPDLVKNKELKTFPPMTSSKPSVD 474
 QY 475 IPNLPSSSSSSFSPYPTSMVTIISIMSSFAIFVLLITTTLYCCRRRKKOMKKRESAY 534
 Db 475 IPNLPSSSSSSFSPYPTSMVTIISIMSSFAIFVLLITTTLYCCRRRKKOMKKRESAY 534
 QY 535 TLTTLPSSELLDRLPNMYQRMPLLNPKLISLEYPRNNIEYVADIGEAGFRYFOARA 594
 Db 535 TLTTLPSSELLDRLPNMYQRMPLLNPKLISLEYPRNNIEYVADIGEAGFRYFOARA 594
 QY 595 PGLLPYEPFTVAAYKMLEEASADMQADFOREALMAEFNDPNYIKLGVCAVCGPKMLL 654
 Db 595 PGLLPYEPFTVAAYKMLEEASADMQADFOREALMAEFNDPNYIKLGVCAVCGPKMLL 654
 QY 655 FEYMAVGDNLNFIKSMSPHTVCSLSHSDLSMPRAQVSSGPPPLSCAEQLCIARQVAAAMA 714
 Db 655 FEYMAVGDNLNFIKSMSPHTVCSLSHSDLSMPRAQVSSGPPPLSCAEQLCIARQVAAAMA 714

715 YLSEKFEVHRLATRNCLVGENMYVVIADFGLSRNIYSADYKANENDAIPIRMMPRESI 774
 717 YLSEKFEVHRLATRNCLVGENMYVVIADFGLSRNIYSADYKANENDAIPIRMMPRESI 776
 775 FYNRYTSDVWAVGVLMELFISYGLQPYGYMAHEVITYYVBDGILSCPEPCPELYNL 834
 777 FYNRYTSDVWAVGVLMELFISYGLQPYGYMAHEVITYYVBDGILSCPEPCPELYNL 836
 835 MRLCWSKLPADRPSTSTHRLIERMCEAEGT 866
 837 MRLCWSKLPADRPSTSTHRLIERMCEAEGT 868
 RESULT 3
 tor-related receptor rtrk - Pacific electric ray
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Torpedo californica (Pacific electric ray)
 D:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
 C:Accession: A47299
 R:Jennings, C.G.; Dyer, S.M.; Burden, S.J.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2895-2899, 1993
 A:Title: Muscle-specific trk-related receptor with a kringie domain defines a distinct c
 A:Reference number: A47299; MUID:93219391
 A:Accession: A47299
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-946 <JEN>
 A:Cross-references: GB:LI1311; NID:9290857; PIDN:AAA49285.1; PID:9290858
 A:Experimental source: electric organ
 A:Note: sequence extracted from NCBI backbone (NCBIN:128724, NCBIR:128726)
 C:Superfamily: Torpedo rtr-related receptor; immunoglobulin homology; kringie homology;
 C:Keywords: ATP; glycoprotein; kringie; phosphotransferase; transmembrane protein; tyros
 E:44-103/Domain: immunoglobulin homology <IM1>
 E:137-195/Domain: immunoglobulin homology <IM2>
 E:229-287/Domain: immunoglobulin homology <IM3>
 F:464-542/Domain: kringie homology <KR3>
 F:572-588/Domain: transmembrane #status predicted <TM>
 F:650-940/Domain: protein kinase homology <KIN>
 F:658-666/Region: protein kinase ATP-binding motif
 F:225,340,477,544/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.4%; Score 2897; DB 1; Length 946;
 Best Local Similarity 59.9%; Pred. No. 8,3e-138;
 Matches 571; Conservative 113; Mismatches 169; Indels 100; Gaps 11;

5 VNIPVLHILTLVAFSGTEK-LPKAFVITPTLETVDALVEEATFMCAYESYQPEISWT 62
 6 VDIPLMLIF-LVTTGSGASGILPKAPQITSPLETVDALVEEASFCVADSYPAAEITWT 64
 63 RKILIKLEDTKSTIRENGOLITLISVEDSDGICCTANNGVAGAVESGALQVMMKPK 122
 65 RNNIPRPETRTYSTKENGOLITLISVEDSDGICCTANNGVAGAVESGALQVMMKPK 124
 123 ITRPPINVKIEGLKAVLPCTTMGNPKPSWIKGDSPLR-EMSRVIAVESSGLRIHNV 181
 125 ITRPPIDVRLGLSKVLPCTTMGNPKPSWIKGDSPLR-EMSRVIAVESSGLRIHNV 184
 182 KEDAGQRCVAKNSLGTAVSKVVKLEFEVFAIRLAPESHNVTFGSEVTLTATGPIPV 241
 185 LEDAGVRCVAKNSLGTAVSKVVKLEFEVFAIRLAPESHNVTFGSEVTLTATGPIPV 244
 242 TTTWINGANAVSSGSIQESQKDVIRDLFTTKPGLYICITNKHGEKFSATAKAT 301
 245 TITWLENGAVPKGSIQNRKIGEMSRRLRVYTRPSLFTCLTNKNESTTAKATATL 304
 302 SIAMSPKQDNKGQYCAQYGCYCNVLAQDALVFLTSTYADPEEAQELVHTAMNELKV 361
 305 DIKEM-RLYKGDIGCTGYGECGGLGNGOLVFNFSRPADEGQEDMARSTWELDG 363
 362 VSPVCPRAEALLCNHIFQECSP-GVVPTRPIPICREYCLAIVKELFCAKEMLVMEKTHRG 420

364 VSLCKPAESELCHFIPODCNPLGLPTPKLVCREHCLAVKELCYKEMITMEDNSRIG 423
 421 LYRSEMHLLSVKCSKLSMHWDPACARPLHD-----YKNENL----- 460
 424 YLSAG--LSLPDCCRLDSIHDPACTGYFLDKKGLVTRMCTYNNNGRYGGSVNTA 480
 461 -----KTPPMTS----- 469
 481 SGISQRMSEQAHPHRRRLPELIFPELANDNCRNPGSESRPMCTYMDROIWECNVP 540
 470 -----KPSVDIPLPSSSSSFSVSPTYSMTVYIISMSFAIFVLLITTYGCC 518
 541 QCINVSISEMKPKTETANTPSTSA-----TYSMTVYIISMSFAIFVLLITTYGCC 593
 519 RRRKMKKK--RESAAVLTLPSELIDRLHPNPMVORMPLNPKLSLEYPRNIE 576
 594 HHQKGLQTKRSYRTETPLATLPSELIDRLHPNPMVORMPLNPKLSLEYPRNIE 653
 577 YVRDIGEGAFGVFOARAPGLLPYEPFTVAVKMLKEASADQADFOREALMAEFDP 636
 654 YVRDIGEGAFGVFOARAPGLLPYEPFTVAVKMLKEASADQADFOREALMAEFDP 713
 637 NIVKLLGVCAVCKPMCLFEYVAYGDLNEFLRSMSPHYVCSLSHSDLSMRAOVSSFGPP 696
 714 NIVKLLGVCAVCKPMCLFEYVAYGDLNEFLRSMSPHYVCSLSHSDLSMRAOVSSFGPP 773
 697 LSCADQLCIAROVAAAMATLSERKFPVHRLATRNCLVGENMYVVIADFGLSRNIYSADY 756
 774 LSCADQLCIAROVAAAMATLSERKFPVHRLATRNCLVGENMYVVIADFGLSRNIYSADY 833
 757 KANENDAIPIRMMPRESIIFYNRYTSDVWAVGVLMELFISYGLQPYGYMAHEVITYYR 816
 834 KANENDAIPIRMMPRESIIFYNRYTSDVWAVGVLMELFISYGLQPYGYMAHEVITYYR 893
 817 DGNITSCPEPCPELYNLMLRCLWSKLPADRPSTSTHRLIERMCEAEGT 869
 894 DGNITSCPEPCPELYNLMLRCLWSKLPADRPSTSTHRLIERMCEAEGT 946
 RESULT 4
 A45082
 neurotrophic receptor ror1 precursor - human
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
 C:Accession: A45082
 R:Maslakowski, P.; Carroll, R.D.
 J. Biol. Chem. 267, 26181-26190, 1992
 A:Title: A novel family of cell surface receptors with tyrosine kinase-like domain.
 A:Reference number: A45082; MUID:93100347
 A:Accession: A45082
 A:Molecule type: mRNA
 A:Residues: 1-937 <MAS>
 A:Cross-references: GB:M97675; NID:9337464; PIDN:AAA60275.1; PID:9337465
 A:Note: sequence extracted from NCBI backbone (NCBIR:120916)
 C:Genetics:
 A:Gene: NTRK1
 A:Cross-references: GDB:136453
 A:Map position: 6p21-6p21
 C:Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringie homology;
 C:Keywords: ATP; glycoprotein; kringie; phosphotransferase; transmembrane protein; ty
 F:4-23/Domain: signal sequence #status predicted <SIG>
 F:24-937/Product: neurotrophic receptor ror1 #status predicted <MAT>
 F:12-133/Domain: immunoglobulin homology <IM>
 F:313-391/Domain: kringie homology <KR>
 F:404-425/Domain: transmembrane #status predicted <TM>
 F:471-753/Domain: protein kinase homology <KIN>
 F:47,66,184,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.7%; Score 899; DB 2; Length 937;
 Best Local Similarity 31.5%; Pred. No. 8,4e-38;

Db 713 CPDDCPAWYALMIECWNEFPSPRRPREKDIHSRL-----RAWGNLS 753


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RESULT 6
S06943
brain-derived neurotrophic factor receptor precursor - mouse
N:Alternate names: receptor tyrosine kinase trkB
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 11-Jun-1999
C:Accession: S06943
R:Klein, R.; Parada, L.F.; Coulter, F.; Barbacid, M.
EMBO J. 8, 3701-3709, 1989
A:Title: trkB, a novel tyrosine protein kinase receptor expressed during mouse neural de
A:Reference number: S06943; MUID:90059970
A:Accession: S06943
A:Molecule type: mRNA
A:Residues: 1-821 <KLE>
A:Cross-references: EMBL:X17647; NID:g55505; PIDN:CAA35636.1; PID:g55506
C:Genetics:
A:Gene: trkB
C:Function:
A:Description: regulation of nervous system development; receptor for brain-derived neur
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
Inase
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
F:32-434/Domain: extracellular #status predicted <EXT>
F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:435-451/Domain: transmembrane #status predicted <TMN>
F:452-821/Domain: cytosolic #status predicted <CYT>
F:535-813/Domain: protein kinase homology <KIN>
F:543-551/Region: protein kinase ATP-binding motif
F:67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Asn) (coval
F:571/Active site: Lys #status predicted
F:706/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
F:816/Binding site: phosphate (Tyr) (covalent) #status predicted
Query Match 18.9%; Score 862; DB 1; Length 821;
Best Local Similarity 28.5%; Pred. NO. 5.2e-36;
Matches 259; Conservative 121; Mismatches 254; Indels 276; Gaps 34;
34 LETVALVEEVATFMCAYESYPOPEISWTRNKLILKLEDTYSIRE-----NQ 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
96 LTIYDSGLKFAVA-YKAFIKNSMLRHINFTRNKL-----TSLSRHFRHLDSLLTGN 148
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
83 -----LTLTIVSDSD--GIYCCTANN--VGAVESGALQVMKPRITRP 126
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
149 PFTSCDIMLKLITQETKSSPTDOLYCLNESSKNMPLANIQIPNGL-----PSARIA 202
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
127 PINVYITIGLKAIVLPCTMGAKPKSVSWTKGD---SPLENSRIAVLESGLRIINVOKE 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
203 APNLVVEGSKSVTLSCSVSGDPLPLLYDVGNLVSKHNMETS---TQGSRLRITNISSD 258
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
184 DAG-QYRCVANKSLGTAVSKV-VKLEFEVFARILRAPESHN---VTFSFVTLHCTANGI 238
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
259 DSGKQISCAVLENVGEDDDSVNLVHFAPTITFLESPTSDDHMCIPF-----TVKCN 310
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 PVPTTIWNGNAVSSGSIQESVKNIDSR---LQLFTTKP-----GLVTCIATNKH 288
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
311 PKPALOMFYNG-AILNESKYICTKIHVNHTEYHGCLQL--DNPTHMNNGDYTLMAKNEX 367
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
289 GEKSTAAATATISIAESKPKQDKKGYCAQYRGVCNAVLAKDLVFLNTSYADPERAQ 348
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
368 G-----KDERQISAHFMG----- 380
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
349 ELVHTVAMELKVSPVCRPAEALLCNHIFQECSPGVVPTPIPICRECYLAVKELFCAK 408
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 -----RPGVD-----YETNP-----NYPEVLVE----- 398

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409 EMLVMEKTHRGILYRESEMLLSVPCSKLPMSHMDPTACARLPHLDYNNKENLTPPMTS 468
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
399 DWT-----PTDIGDPT-----NKS----- 414
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
469 SKPSVDIPNLPSSSSSFSVSPTYSMTYIISMSFAIFVLLITTLTYCCRRKKOKNKK 528
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
415 ELPSTYVAD--QSNRHLVY---YAVVYIASVY---FCLVMLLLKLARKSKFGMKG 465
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
529 RESAAVTLTTPSELLDRILHNPMTQ-----RMLPLNPKL 565
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
466 PASV-----ISNDSDASPLRHINISGNTSPSSSGGPDVAIIGMTKIPVNIENPQY 515
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
566 LSL-----EYRNINIEYVADIEGAFGRFGQARACGLLYEPPTMYAVVMKLE 613
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
516 FGITNSQLKPDITFVQHIKKNHNTYLLKKELEBGAFGKFLACVYLCEPOKILVAVUTLK- 574
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
614 EASADQADFOREAALMAEFNDPNIVKLGVCVAGKPMCLLPFYMAVYGLDNEFLRSMSPH 673
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
575 DASDNARKDPHREBELTTLMLQEHYKFGVCYEGDPLINVFYMKHGLNKLRAHCPD 634
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
674 TVCSLSHSDLSMRAQVSSGPP--LSCAEQLCIARQAVAGNAYLSERKFVHNDLATRNC 731
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
635 AV-----LMAEGNPTELQSQMLHIAQIAGWVYIASQFVHRDLATRNC 681
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
732 LVGENNVYKIADPGSRNITYSDYKANKENDAPIITWMPRESIFVRYRTTESVMAVGV 791
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
682 LVGENLVVITIGDGRSDYSTDYRVGHTMPLIKMMPBESTIMRKFTTESVWSLVGV 741
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
792 LWEIFSYGLQPYGMAREVIVYVRDGNILSCPENCPVELYMLMLRCLMSPADRSFVS 851
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
742 LWEIFSYGLQPYGMAREVIVYVRDGNILSCPENCPVELYMLMLRCLMSPADRSFVS 801
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
852 IIRILERMCE 861
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
802 IHTLLQNLAK 811
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 7
A56853
brain-derived neurotrophic factor receptor precursor - human
N:Alternate names: receptor tyrosine kinase trkB
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 11-Jun-1999
C:Accession: A56853; I56557
R:Nakagawa, A.; Liu, X.G.; Ikegaki, N.; White, P.S.; Yamashiro, D.J.; Nycum, L.M.;
Genomics 25, 538-546, 1995
A:Title: Cloning and chromosomal localization of the human TRK-B tyrosine kinase rece
A:Reference number: A56853; MUID:95309922
A:Accession: A56853
A:Molecule type: mRNA
A:Residues: 1-822 <NAK>
A:Cross-references: GB:U12140; NID:g525313; PIDN:MAC51371.1; PID:g530791
R:Shelton, D.L.; Sutherland, J.J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H
J. Neurosci. 15, 477-491, 1995
A:Title: Human trks: molecular cloning, tissue distribution, and expression of extrac
A:Reference number: I56557; MUID:95123473
A:Accession: I56557
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-822 <SH>
A:Cross-references: GB:S76473; NID:g913717; PIDN:AAB33109.1; PID:g913718
C:Genetics:
A:Gene: trkB
A:Cross-references: GDB:127898; OMIM:600456
A:Map position: 9q22.1-9q22.1
C:Function:
A:Description: regulation of nervous system development; receptor for brain-derived n
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fac
F:1-31/Domain: signal sequence #status predicted <SIG>

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F:32-822/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
 F:32-435/Domain: extracellular #status predicted <EXT>
 F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:436-452/Domain: transmembrane #status predicted <TM>
 F:453-822/Domain: cytosolic #status predicted <CYT>
 F:536-814/Domain: protein kinase homology <KIN>
 F:544-552/Region: protein kinase ATP-binding motif
 F:67,95,121,178,205,241,254,280,335,338,350,412/Binding site: carbohydrate (Asn) (covalent)
 F:572/Active site: Lys #status predicted
 F:706/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 F:817/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 18.8%; Score 861; DB 1; Length 822;
 Best Local Similarity 29.5%; Pred. No. 5,9e-36;
 Matches 253; Conservative 115; Mismatches 269; Indels 222; Gaps 30;

59 ISWTRKILKLPDTRYSIRENGQL-----TILSVSDSD--GIYCCT 100
 120 INFTRK-LTSLSKHRRHDLSELILVGNFTCSCLMKTITQEAQSSPDODICLN 178
 101 ANNG-----VGGAVESGALGVKMKPKITRPINKIIEGLKAVLPCTTMGPKPSVSWIK 156
 179 ESSKNIPLANQIPNCGI-----PSANLAPNLTVBERGKISITLSCVAGDPVPMWDV 232
 157 GD---SEPREKRIAVLESGLRIHNQKEDAG-QYRKVANSGTAVSKV-VKLEPEVF 211
 233 GNLSVKHNNETSH---TQGLRITNISSDSGKQISCAVNLGVEDDVSNLVTHFAPT 288
 212 ARIAPRESH---VTFGSEFTLCTATGIPVPTITMENAVSSGSIQESVDRIADS 268
 289 ITFLESPTSDHMKIPF-----TYKGNPKPALQWYNG-ALINEKYLCTIHLHTNH 339
 269 R-----IQLFTKP-----GLYCIATNKHG-EKFSATAAATISAEWSKPO-----K 311
 340 TEYHGCIQL--DNPTHMNGDYTLIAKNEYGKQISAHMCGMVGIDDGNPNVPIY 397
 312 DNKQICAOYRGVGNNAVIAKALVFLMYSVADPEAQELVHTMNLKLVSPICRAPE 371
 398 EDVGTANDIGDTTNR-----SNEIPSTDVTKGRELISYAVAVIASVG----- 444
 372 ALLCNHIFQESGCVVPVPIPIPCREYCLAVELCAKEMWEMERTHGLRSEMHLSV 431
 445 -----FCL-----LVM-----LFLKL 456
 432 PKCSKL---PS--MHMDPTACARLPHLDVKNEMLKTFFPMTSSKPSVDIPLNLSSSSS 485
 457 ARHSKFGKGPASVYSINDDSASPLNHSNGS-----NTPSSSSEG 497
 486 FSVSPYTSMTYIISMSFAIFVLLTTTLCRRRQKMKKRESAVALTTLTPSELL 545
 498 -----PDVYIGMTKP----- 509
 546 DRLHPNPTQMP-LLNPKLLSEYPRNNIEYVDIGEGAFGRVQARAGLLPYEPT 604
 510 --VIENPOYFGITNSQLKPFDFYQHKKRHNIYVLRKELEGCAFAGKFLAECYNLCPEODKI 567
 605 MVAAYKMLKEESADMOADFOREALMAEFDPNIVYKLLGVCAVGRPKMLLEFYAAGDNL 664
 568 LVAAYTKL-DASDNARKKFRHREALLTNLQHEHIVKFGVCEVGDPLLMVEYMKHGLN 626
 665 EFLSMSPHTYCSLSHSDLSKRAOVSSPGPP--LSCAEQICIAROVAAGAAVYSERFV 722
 627 KFLAHAGPDAY-----LMAEGNPTELITQSOMHIAQIAGAVVYIASQHFV 673
 723 HRDLATRNCLVGENMVYKIADEGLSRNYSADYKANKENDALPIRMPDPESIFNRYTTE 782
 674 HRDLATRNCLVGENMLVYIGDFGMSRDYVSPDYRVGQHTMLPIRMPDPESIMYRKFTTE 733
 783 SDVAYGVVLMETISYGLQPIYGAHAEVITYVDGNILSCPENCPVELLYMLRLCWSKL 842

DB 734 SDVMSLGVLMETIPTYKOPYQLSNNEVEICITQGRVLOPRPCQVEYELMGQORE 793
 QY 843 PADRPSTSIHRIEMCE 861
 DB 794 PHMKRNKIGHTLQNLAK 812

RESULT 8
 S44098
 brain-derived neurotrophic factor receptor precursor - chicken
 N:Alternate names: receptor tyrosine kinase trkB
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Jan-1995 #sequence, revision 13-Jan-1995 #text_change 11-Jun-1999
 C:Accession: S59939; S42175; S44098
 R:Vinh, N.O.; Erdmann, K.S.; Heumann, R.
 Gene 149, 383-384, 1994
 A:Title: Cloning and sequence analysis of a cDNA encoding a novel truncated form of t
 A:Reference number: S59938; MUID:95047511
 A:Accession: S59939
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-818 <VI2>
 A:Cross-references: EMBL:X77251; MID:9563881; PIDN:CA54468.1; PID:9472934
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
 R:Dechant, G.; Biffo, S.; Okazawa, H.; Kolbeck, R.; Pottgiesser, J.; Barde, Y.A.
 Development 119, 545-558, 1993
 A:Title: Expression and binding characteristics of the BDNF receptor chick trkB.
 A:Reference number: S42175; MUID:94116452
 A:Accession: S42175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-818 <DEC>
 A:Cross-references: EMBL:X74109; MID:9407798; PIDN:CA542210.1; PID:9407799
 C:Genetics:
 A:Gene: trkB
 C:Function:
 A:Description: regulation of nervous system development; receptor for brain-derived n
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc
 C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fact
 inase

F:31/Domain: signal sequence #status predicted <SIG>
 F:32-818/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
 F:32-432/Domain: extracellular #status predicted <EXT>
 F:66-90/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:115-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:138-149/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical
 F:433-449/Domain: transmembrane #status predicted <TM>
 F:450-818/Domain: cytosolic #status predicted <CYT>
 F:530-810/Domain: protein kinase homology <KIN>
 F:540-548/Region: protein kinase ATP-binding motif
 F:66,94,120,199,204,253,287,324,337,349,408/Binding site: carbohydrate (Asn) (covalent)
 F:568/Active site: Lys #status predicted
 F:702/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi
 F:813/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 18.8%; Score 858; DB 1; Length 818;
 Best Local Similarity 29.4%; Pred. No. 8.2e-36;
 Matches 262; Conservative 118; Mismatches 281; Indels 230; Gaps 35;

6 NIPLVHT-LTLVAVSGTKLPRAPYITPLETVDALVEVATFMCVAVSYQPEISWTRN 64
 DB 113 NINLIYIMLSRNKLSLSKKPFRIHGLDLIVD-----NPFKSC-----ELMWIK- 159
 QY 65 KILKLPDTRYSIRENGQLLILSVSDSDGTYCCTANNNGVAGAVESGALGVKMK----- 120
 DB 160 ---KFOETKK-----YTEAOD--IYCDVNN-----KRALMDMKVFNCDL 195
 QY 121 PKTRPPINVKIIEGLKAVLPCTTMGPNKPSVSWI-----KQSPLENSRIAVLESGLS 174

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Db 196 PSANISNITIVYEGSKITLYCDTGGPPPNVSWLTJNLVNSHESDTSKN-----PAS 248
Oy 175 LRIHNVQKEDAGQY-RCVAKNSLGTAYSKYVKLEFEVFARILRAPESHVTFGSEYTF--- 230
Db 249 LTIKNVSSDGLMISCAVENIVGEVQISA-----ELTVF-----AP---NITILESTTPH 298
Oy 231 ---LHCTATGIVPPTIWIENGNAVSSGISQGSVDRIISR-----IQLETTKP----- 277
Db 299 HWCIFETVGNKPTLQWVEEG-ALLNESEYICTKIHVINOSEYHQCQLD--DNPTHLNN 355
Oy 278 GLYTICATNKHGKSTKAAATISAEKSKQKONKGCACAYR---GEVCNANVLAKDL 334
Db 356 GAVTLAKKEGE-----DEKRVDAHFMSVPGSGSPIDDPDY 394
Oy 335 VFLNTSVADPEEAQELLVHTANNEKLVSP-VCPRAAEALLCNHIFQECSPGVPTPIPI 393
Db 395 EYETI-----PND-----LQGTNNNSNOITSPDYSNKNENESTIVYV-----VCGIALV 439
Oy 394 CREYGLAVKELFCAKEMLVMEKTRGLYRSEMHLISVPKSKLPS--MHMDPTACARLP 451
Db 440 CTGLVIML-----IILKGRH-----SKFGM-----KGFSSVISNDODSAPLH 478
Oy 452 HLDYKKNELKTPPMTSSKPSVDIPNLDPSSSSSFVSPTYSMTVIISIMSSFAIFVLLT 511
Db 479 HISNGS-----NTFSSSEGC-----493
Oy 512 ITTLVCCRRRQWKKKRESAAVLTTLTLPSELLDLRHPNMYQRM-LLNPKILSLEY 570
Db 494 -----PDAVITGMTKIP-----VIENPOYFGITNSQLKPDTFVOHI 529
Oy 571 PRNIEYVRODIGEAFGVFOFARGLLPERPTVAVKMKLEKESADMQADFOREBALM 630
Db 530 KRNHIVLKRLEGEAFGVFVLAECYNLCPEODKILVAVKTK-DASDNARKGFHREBEL 588
Oy 631 AEFDPNIVKLGVCAVGRKPCMLFEYMAVGDLEFLRSMSPHTYCSLSHSDLSMAQVS 690
Db 589 TNLQHEHIVKFGYCVESDPLIMVEFYMKHDLNKFRAHGRDAV-----LMAE 637
Oy 651 SPGRPLSCAEQDLCTAROVAAAGMAYLSERKRVHDLATRNCLVGENNVYKADFGLSRNI 750
Db 638 GNRPELLOSOMLHTAOOIAAGMVYLAHQFVHDLATRNCLVGENNLYVKIDFGMSRDY 697
Oy 751 YSADYKKNENDALPIRMMPRESIFYNRYNTTESDVAAGVYVMEFESGLQGYGMAHDE 810
Db 698 YSTDYIRKGGHTMLPIRMMPRESIYRKFTTESDVSGLVYVMEFETGKQDPWYOLSNE 757
Oy 811 VIVYVRDGNILSCPENCPVELYNLMRLCWSKLPADRPSTSIHRIERKCE 861
Db 758 VIECTIGRVLQRPRTCPKEYVDLMLGCMQRPNRLNIKEHSLQLNIAK 808

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RESULT 9
A39667 brain-derived neurotrophic factor receptor precursor - rat
N:Alternate names: receptor tyrosine kinase trkB,FL
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Nov-1991 #sequence,Leviston 27-Nov-1991 #text,change 11-Jun-1999
C:Accession: A39667
R:Middlemas, D.S.; Lindberg, R.A.; Hunter, T.
Mol. Cell. Biol. 11, 143-153, 1991
A:Title: trkB, a neural receptor protein-tyrosine kinase: evidence for a full-length and
A:Reference number: A39667; MUID:91094826
A:Accession: A39667
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-821 <MID>
A:Cross-references: GB:M55291; NID:g207473; PIDN:AAA42279.1; PID:g207474
C:Function:
A:Description: regulation of nervous system development; receptor for brain-derived neu
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
inase

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F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
F:32-434/Domain: extracellular #status predicted <EXT>
F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:92-113/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:435-451/Domain: transmembrane #status predicted <TMN>
F:452-821/Domain: cytosolic #status predicted <CTT>
F:535-813/Domain: protein kinase homology <KIN>
F:543-551/Region: protein kinase ATP-binding motif
F:67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Asn) (cov
F:571/Active site: Lys #status predicted
F:705/Binding site: phosphate (Tyr) (covalent) #status predicted
F:816/Binding site: phosphate (Tyr) (covalent) #status predicted

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Query Match 18.7%; Score 854.5; DB 1; Length 821;
Best Local Similarity 28.3%; Pred. No. 1,2e-35;
Matches 249; Conservative 113; Mismatches 254; Indels 263; Gaps 30;

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Oy 59 ISWTRNKILIKLFDTRYSIRE-----NGQ-----LLTILSVESDSD--G 95
Db 120 INFTRNKL-----TSLSRHFRHLDLDLITGNPFQSCDIMLKTQLQETKSSPDQD 173
Oy 96 IYCCTANNQ-----VCGAVESGALQVKKMKITRPPIYKIIIEGLKAVLPCTMGPKPS 151
Db 174 LYCLNBSKNTPLANLQIPNGL-----PSARILAPNLTVLEGKSVTISCVGCDPLPT 227
Oy 153 VSWIGD---SPLRENSRAVLSESGLRHNVQKEDAG-QYRCVAKNSLGTAYSKV-VKL 206
Db 228 IYWDVGNLVSKMNETSH---TQGLSRITNTSSDSCQKQICVAVENLGEODSDSVNLTV 283
Oy 207 EEFVFARILRAPESHN---VTFGSEVTLHCTGTGIVPPTIWIENGNAVSSGISDESVD 263
Db 204 HCAPITPLESTSDHNCIFP-----TYRGNPKPALQWFGNG-ALLNESKIYCTKI 334
Oy 264 RVIDSR-----IQLEITKP-----GLYTCIATNKHGE-----KFTAKAA 298
Db 335 HVTNTEHYGCLQ--DNPTHMNGDYTLMAKNEXGKDERQISAHFMGRPGVDYENPAY 392
Oy 299 ATISIAENSKP-----QDNKGYCAQYRGVCNANVLAKDLVFLNNTSYADPEEAQELL 351
Db 393 PEVLIEDWTTPDIDGDTTKNSNE-----IPSDVADAOJTRNHL 431
Oy 352 VHTANNEKLVSPVCPRAAEALLCNHIFQECSPGVVPTPIPICREYCLAVKELFCAKEL 411
Db 432 YVAVVVIASVVG-----FCLLVML-----451
Oy 412 VMEKTRHGLYRSEMHLISVPKSKL---PS--MHMDPTACARLPNLDYKNENIKTPRP 465
Db 452 -----LKLARHSKFGMKGPASVISNDODSAPLHISNGS-----487
Oy 466 MTSKPSVDIPNLDPSSSSSFVSPTYSMTVIISIMSSFAIFVLLTITLTYCCRRKQK 525
Db 488 -----NTFSSSEGC-----496
Oy 526 NKKRESAAVLTTLTLPSELLDLRHPNMYQRM-LLNPKILSLEYPRNIEYVRODIGEG 584
Db 497 ---PDAVITGMTKIP-----VIENPOYFGITNSQLKPDTFVOHIKRNHIVLKRLEGB 546
Oy 555 AFGRFQARAGLLPERPTVAVKMKLEKESADMQADFOREBALMAEFDNPNIYKLLGV 644
Db 547 AFGKVFLEACYNLCPEODKILVAVKTK-DASDNARKGFHREBELTJNLQHEHIYKFGV 605
Oy 645 CAVGRKPCMLFEYMAVGDLEFLRSMSPHTYCSLSHSDLSMAQVSSGPRP--LSCAEQ 702
Db 606 CVEGDPLTIVFEYMKHGLNKFRAHGRDAV-----LMAGNDPTLTJQSDM 652
Oy 703 LCIAROVAAAGMAYLSERKRVHDLATRNCLVGENNVYKADFGLSRNIYSADYKANEKD 762
Db 653 LHIQOIAAGMVYLAHQFVHDLATRNCLVGENNLYVKIDFGMSRDYISTDYIRKGGHT 712

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QY 763 AIPRMPPESTFYNNRTTESDWMAYGVLMETFSYGLQPYGMAHEEVIYYVNDGNIIS 822
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 713 MIPRMPPESTFYNNRTTESDWMAYGVLMETFSYGLQPYGMAHEEVIYYVNDGNIIS 822
QY 823 CPENCPEVELYNLMRLCWSKLPADRPSTSIHRLIERMCE 861
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 773 RPRTCPOVEYELMGLGCMQREPHFRKRNKNTHTLQNLAK 811

RESULT 10
A39712
kinase-like protein klg precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999
C:Accession: A39712
R:Chou, Y.H.; Hayman, M.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991
A>Title: Characterization of a member of the immunoglobulin gene superfamily that possib
A:Reference number: A39712; MUID:91271300
A:Accession: A39712
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1051 <CHO>
A:Cross-references: GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP
F:775-1046/Domain: protein kinase homology <KIN>
F:783-791/Region: protein kinase ATP-binding motif

Query Match 18.2%; Score 833; DB 2; Length 1051;
Best Local Similarity 27.7%; Pred. No. 1.9e-34;
Matches 242; Conservative 150; Mismatches 310; Indels 172; Gaps 31;

QY 26 KAVYITPLETVVALVEVATF-----MCAN-ESTPQPEISTRTKILIKLF 71
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 290 KALVLAATLTLAE--IEEMAFSPKYLTLANOGRHVSACPRGVPTPOVWMEKNO---ERV 344
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 72 DFRSIRENQLTLTILSVESDGIYCTANNGVGAVERGALQVAKRKTRPPINVK 131
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 345 PTAGRYQAEMLVFTSITADAGIYCHANKANGKEKKQEL-SITVATVTKWVEMPDSQ 403
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 132 ITIGLAVALPCTTMGNPKPVSWSIKGDSPLRENSRIAVLESGRIHNVOKEDAGYRCV 191
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 404 LBSKPKYIHLCKSKALPKVTWYRNGVSISEDSREISNGTLRINNVEYDGTMYKCV 463
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 192 AKNSLIG--AYSKV---VKLEFEVFAILIRAPESHNVTFGSEFVLIHCTATGIPPTTWI 246
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 464 SSTPAGSIEGTARYHLEKLTFTPPPOPLQME-----FNKEVTVSCSATGREKPTQWT 518
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 247 ENGNAAVSSGSIQSVKDRV-IDSRLOLEITRPGLYTCIATNK-HGEKSTAKAATISIA 304
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 519 K-----TGGSLSPSHVSRAGILSPHKVSRSDSGNYTCIASNSPGCIRATVQVLVAVYVT 574
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 305 EWSKPKQDN--KGYCAQYREVCNAVAKALVPLNTSYADPREAQELLYHTAM-NELKV 361
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 575 FKEPEPTTYVQGHYAFQ---COA-----EGDP-----VPHIQWKGKDKI 612
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 362 VSPICRAAALLCNHIFFGCSPGVPTPIPICREYCLAVKELCAKEMVMEKTRHGL 421
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 613 LDP----- 615
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 422 YRSEMHLLSVKCSKLPs---MMMDPTA-CARLLPHLDYKNELKTERPM-TSSKPSVD 474
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 616 --SKL---LPRIQIMNGSLIVYDTTSDSGKYTCIAGNSCNIKHREAFLLVVDKPAAE 669
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 475 IPNIPSSSSSSFSVSPYYSM--IYIISMSFAFVLLITTLTCCRRRQWKKKR-ES 531
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 670 EDEPSSHT-----PYKMIQTGLSVGAAYVITIIIVLGMFCRKRRAKRLKKHDEG 722
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 532 AAVITLIPSEILLDLRHPNPMYQRMPLLNPKILS-----LEYPRNIEVVRD 580
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 723 EPEMECLNGTLLQNOOTTAIEIOEVALTNLSSSGASKRHSARMDMHPFRSLQITTT 782

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QY 581 IGGAGRGVQARAPGLLEPPTVAVKMLKEASADMOADPQREAAALMAEFDNPIVK 640
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 783 LGRGEFGEVFLAKAKGAEADGALVLYKSL-OTRBEQLOLDRRREKMGKLNHNVR 841
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 641 LIGVCAVGRKPMCLLFEYMAAGDNEFLRSNPHPTVCSLSHS-DLSMRAQVSGPPPLSC 699
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 842 LIGLCREAREPHVWVLEVDLDGLKQFLR-----ISKKDESLK-----PQPLST 885
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 700 AEOLCTARQYAAAGMAYISEKFEYHRDLATFNCLVGENMNVYKIADFGLSRNIYSADYYKAN 759
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 886 KHNVSLOTQVALGMEHLSNRFVHRDLAARNCLVASQROYKVALSLSKDVYNSETHFR 945
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 760 ENDAIPRMPPESTFYNNRTTESDWMAYGVLMETFSYGLQPYGMAHEEVIYYVNDG 819
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 946 Q-AMIPLRMPPEAVLEDESTKSDVMSFGVLMMEVFTQEGEMPYAPLADEVLAGKSGK 1004
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 820 I-SCPENCPEVELYNLMRLCWSKLPADRPSTSI 852
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1005 TKLPQEGCPSRLTKLMQRCMAFSPKDRPSTSEL 1038
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
THOUT
nerve growth factor receptor precursor, high affinity - human
N:Alternate names: receptor tyrosine kinase trka
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 11-Jun-1999
C:Accession: A30124; S02366; A25184
R:Martin-Zanca, D.; Oskam, R.; Mitra, G.; Copeland, T.; Barbacid, M.
Mol. Cell. Biol. 9, 24-33, 1989
A>Title: Molecular and biochemical characterization of the human trk proto-oncogene.
A:Reference number: A30124; MUID:89181575
A:Accession: A30124
A:Molecule type: mRNA
A:Residues: 1-790 <MAR1>
A:Cross-references: GB:M23102; NID:g339917; PIDN:AAA36770.1; PID:g339918
R:Kozma, S.C.; Redmond, S.M.S.; Xiao-Chang, F.; Saurer, S.M.; Groner, B.; Hynes, N.E.
EMBO J. 7, 147-154, 1988
A>Title: Activation of the receptor tyrosine kinase domain of the trk oncogene by recombination
A:Reference number: S00261; MUID:88196074
A:Accession: S02366
A:Molecule type: mRNA
A:Residues: 393-758; 'HG', 761-790 <KOT>
A:Cross-references: EMBL:X06704; GB:V00100; NID:g37399; PIDN:CAA29688.1; PID:g37400
R:Martin-Zanca, D.; Hughes, S.H.; Barbacid, M.
Nature 319, 743-748, 1986
A>Title: A human oncogene formed by the fusion of truncated tropomyosin and protein t
A:Reference number: A25184; MUID:86146854
A:Accession: A25184
A:Molecule type: mRNA
A:Residues: 393-762; 'SNATASRMCTPGCKPMPRHLLSTWMSWARGPAGLGVSRNTGACDPHP' <MAR2>
A:Cross-references: EMBL:X03541; NID:g37402; PIDN:CAA27243.1; PID:g37403
A>Note: the difference at the carboxyl end is due to a frameshift
C:Comment: The proto-oncogene trka is activated by gene fusion. The amino end of seve
C:Genetics:
A:Gene: GDB:NTRK1; TRK
A:Cross-references: GDB:127897; OMIM:191315
A:Map position: 1q21-1q22
C:Function:
A:Description: regulation of nervous system development; receptor for nerve growth fa
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc
C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphopr
ectic protein kinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-70/Domain: nerve growth factor receptor, high-affinity #status predicted <MAT>
F:33-415/Domain: extracellular #status predicted <EXT>
F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical
F:416-432/Domain: transmembrane #status predicted <TMN>

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F:433-790/Domain: cytosolic #status predicted <Cyt>
 F:502-782/Domain: protein kinase homology <Kin>
 F:510-518/Region: protein kinase ATP-binding motif
 F:67,95,121,188,202,253,262,281,318,323,338,358,395/Binding site: carbohydrate (Asn) (cc
 F:538/Active site: Lys #status predicted
 F:674/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 F:785/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 17.7%: Score 810; DB 1; Length 790;
 Best Local Similarity 27.3%: Pred. No. 2e-33;
 Matches 254; Conservative 116; Mismatches 257; Indels 304; Gaps 29;

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QY 1 MRELVIPIVHITLV-----AFSGTEKLPKAPVITTPLETVDALVEEATFMCA 50
DB 84 LNDLRGLGRLNLTIVKSGSLRFVAPDAFHTPLRLNLSFNALSS----- 129
QY 51 VESYPPQETSWTRNKILKLFDRYSIRENGQLTILSLEDSDGITYCTA-----N 102
DB 130 -----LSW-----KTVOGLSLQELVLSGNPLHSCALRMILQRMEE 164
QY 103 NCVGGAVE-----SCGALQYKMKPKITRPINVKIIEGLKAVLPCTM 145
DB 165 EELGVPEQKLCQHGCGPLAHMPNASCQVPLTKQYR-----MASVDGDDVILRCQYE 218
QY 146 GMPKPSVMIKGDSPLENSRIA-VLESG-----SLRINVOKE-DAGQYRCVAKNSLGT 198
DB 219 GGLGLEDAGMI-----LTLEQSATYKSSGSLPSLGLTLNANVSDLRKMLTGWAEVDGR 273
QY 199 AVSKVVKLEFEVFAIRILRAPESHNTFGSFVTLHC-----TAGGIYPTITWIE 247
DB 274 A-----EVSQV-----NSFPASVOLHRAVENHMSIPESVDGQAPRLWLF 317
QY 248 NCVNAVSSGS-----IQESVKDRVIDSRQLFTKPR-----GLTYCIATNKGEKSTAK 296
DB 318 NCSVNIENSFITEEFLEPAANETVRHGCRL--NQPTHVNGNITLLANPPGQ----- 369
QY 297 AATISIAEMSKRQKDNKCYCAQYGEVCNANVLADALVFLWTSIADPEAOELLVHTAM 356
DB 370 ASASIMAFMDNPFEFN-----PDDPIPTDSTSGDPEKKD----- 406
QY 357 NELKVVSPVCRPAEALLCNHIFQCSPCGVPTPIPICHREYLAAYKELCAKEMLVMEK 416
DB 407 -----ETPFGVSAVGLAV--FAC----- 423
QY 417 THRGLYRSEMILLSPKCSKLPMSHMDPTACARLPHLDYKNKENLTFEPMTSSKPSVDIP 476
DB 424 -----LEFLSTL-LLVLNKCGR-----RNKFGI-----NRDAVLAP 452
QY 477 NLPSSSSSSF-----SVSPYKMTVIISIMSPAFIVLTTITTLTXCCRRKQMKKKRE 530
DB 453 EDGLAMSLHFTLGGSSLSPTGG----- 475
QY 531 SAAVTLTLTLPSELDRHPMPYQRMPLLNPKLLSLEYPRNNITEYRIDEGAGFGRVF 590
DB 476 -----KSGGLQGHITIEENPOYTSDACVNHIK-----RQDLYLKWELEGEGAFGVVF 519
QY 551 QARAGCLLYPERFTWVAVKMLKEASADQADFOREAAALMAEFDPNITVKLGLGVCAVGR 650
DB 520 LAECNHLPEREDKMLYAAVKALK-EASESARQDFOREAELLTMLOQHILYRFGVCTEGRP 578
QY 651 MCLFEYAAUGDNLNFFLSMSRPHYCSLSHDSLSRAOVSSGPPPLSCAEOLCIAROVA 710
DB 579 LLMVFEYRRHDDLNFLKSHSP-----DAKLAGEEDVAPQDLGOLLAAVASQVA 629
QY 711 AGMAVLSERKFEVHRDLATRNCLVGENMVVKIADFGLSRNITSAADYKANKENDAPIRMP 770
DB 630 AGMYVLADLHNVHDLATRNCLVQGLVYKIGDGMASDITSTDYRKGAGTMDLDIRMP 689
QY 771 PESIFYNNTTESDVMAVGVVLMETFSYGLQPYGMAHEEVIYVVRDGNILSCPENCFVE 830
DB 690 PESILYRKFTTESDVMSFGVVLMEIFTYGKOPWQLSNTAIDCTQGRELERPRACRPE 749

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QY 831 LYNLMRLCWSKLPADRPSTSIHRIERMC 861
 DB 750 VTAIMRCQWREPQORHSIKDVHARLQALAQ 780

RESULT 12
 S35695

neurotrophin-3 receptor precursor - chicken
 M:Alternate names: receptor tyrosine kinase trkC
 N:Containts: protein-tyrosine kinase (EC 2.7.1.112)
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Dec-1993 #sequence_revision 03-Nov-1995 #extl_change 11-Jun-1999
 C:Accession: S35695
 R:Okazawa, H.; Kamel, M.; Kanazawa, I.
 FEBS Lett. 329, 171-177, 1993
 A:Title: Molecular cloning and expression of a novel truncated form of chicken trkC.
 A:Reference number: S35695; MUID:93359043
 A:Accession: S35695
 A:Molecule type: mRNA
 A:Residues: 1-803 <OK>
 A:Cross-references: EMBL:X59669; NID:9416429; PIDN:CAA42202.1; PID:9416430
 A:Note: the authors translated the codon AAC for residue 105 as Val, CTG for residue
 C:Function: regulation of nervous system development; receptor for neurotrophin-3
 A:Description: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc
 C:Superfamily: alternative splicing; ATP; autophosphorylation; brain; glycoprotein; grow
 C:Keywords: otein kinase
 F:1-10/Domain: signal sequence #status predicted <Sig>
 F:11-803/Product: neurotrophin-3 receptor #status predicted <Ant>
 F:11-417/Domain: extracellular #status predicted <Ext>
 F:58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRI>
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRI>
 F:107-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRI>
 F:130-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRRI>
 F:435-803/Domain: transmembrane #status predicted <TM>
 F:514-795/Domain: cytosolic #status predicted <Cyt>
 F:522-530/Region: protein kinase ATP-binding motif
 F:47,51,58,142,182,197,211,238,246,251,273,354,367/Binding site: carbohydrate (Asn) (cc
 F:550/Active site: Lys #status predicted
 F:687/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi
 F:798/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 17.7%: Score 810; DB 1; Length 803;
 Best Local Similarity 27.4%: Pred. No. 2e-33;
 Matches 221; Conservative 101; Mismatches 214; Indels 270; Gaps 21;

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QY 121 PKITRPINVKIIEGLKAVLPCTMGKPKSVSWIKGD---SPLENSRIAVLESGSLR 176
DB 189 PEISVSHVNLIVREGENAVITCNGSGSLPDDVMTVADLHSINTHTQNLNMTHNAINLT 248
QY 177 IHNQKEDAG-QYRCVANKSLCTAASKVYKLEFEVFAIRLAPR-----SHAVTGSFVT 230
DB 249 LVNVTSEDNGELLTCTIAENVGMSNAVL-LTVYVPRILTLLEBPVLIHLEHCIAF---A 303
QY 231 LHCTATGIPVPTIWIENGNV-----SSGSIQESKDVINDVSRQLDFTKPR-- 277
DB 304 VH-----GNPAPRTLHLNHCQVILRETEIIMERYOQGEVSEGC-----LLENKPTN 349
QY 278 ---GLTYCIATNKHGEKSTAKAATISIAEMSKRQKDNKCYCAQYRGEVCNAVLAKDAL 334
DB 350 YNNGNYTIVATNQLGSANQITKG----- 372
QY 335 VFLNYSADPBEAOGLLVHTAMNELKVYSPVCRPAEALLCNHIFQCSPCGVPTPIPIC 394
DB 373 ----- 372
QY 395 REYCLAVALKELCAKEMLVMEKTHRGLYRSEMILLSPKCSKLPMSHMDPTACARLPHLD 454
DB 373 -----HLEKRP----- 378
QY 455 YNKENLKTFPMTSSKPSVDIPNLPSSSSSSFVSPTYSMTVI-----ISIMSFA 505

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Db 379 -----PESTDNFVSI-----GDYVSPPTLTTHKPEDTFGSIANGLA 420
QY 506 IFVLLITLTYCC-----RRRKQWKN-----KRESAAVLTLPSELLDLRLHPNM 553
Db 421 AFACVLLVFLIMINKYGRSKFGMKGPVAVISGEEDSAHTSTDTREFTD-AGPDV 479
QY 554 ----YQRPDLLNKLISLEY-----FRNNIEYVRDICEGAFGVFQARAGLL 598
Db 480 VIGMTRIPIVENPOYERQGNCHRPDTYYOHIKRDIKRLRELGEAGFVLAECYNLS 539
QY 599 PYEPFTVAVKMLKEEASDMOADFOREALMAEFDPNPIVTKLLGVAVKPMCLPEYM 658
Db 540 PTDMKMLVAVKALKDPLLA-ARKDFOREALLTNLOHEHIYKFGYCGDDPLIMVEYM 598
QY 659 AYGDLEFLRSMSPHTVCSLSHSDLSMRAQVSSPP-----PLSCAEQLCIARQVAA 713
Db 599 KHGDLNKLRAHGPD-----AMILVDGQPROAKGELGLSOMLHIASQIASGM 645
QY 714 AYLSERKFEVHRDLATRNCLVGENNVYKIDPGLSRNITYSADYKANKENDAPIRMMPES 773
Db 646 VYLAQHFEVHRDLATRNCLVGENNVYKIDPGLSRNITYSADYKANKENDAPIRMMPES 705
QY 774 IFYRNTTESDVNAVYGVVLEISYGLQPYGYMAHEEVIYVRDGNILSCPEPCVELYN 833
Db 706 IMRKFTTESDVNAVYGVVLEISYGLQPYGYMAHEEVIYVRDGNILSCPEPCVELYN 765
QY 834 LMRCLMSKLPADRPSTSIHRILEM 859
Db 766 IMLGCCQREPOQLRIKEIKYLIAL 791

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RESULT 13

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A:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Jun-1999
C:Accession: A55178
R:McGregor, L.M.; Baylín, S.B.; Griffin, C.A.; Hawkins, A.L.; Nelkin, B.D.
Genomics 22, 267-272, 1994
A:Title: Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignment, a
A:Reference number: A55178; MUID:95104834
A:Accession: A55178
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-825 <MCG>
A:Cross-references: GB:005012; NID:g442389; PIDN:AAA75374.1; PID:g442390
C:Genetics:
A:Gene: GDB:NTRK3
C:Cross-references: GDB:127899; OMIM:191316
C:Map position: 15q24-15q25
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycoprotein
C:Keywords: alternative splicing; ATP; growth factor receptor
F:79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR4>
F:536-817/Domain: protein kinase homology <KIN>
F:544-552/Region: protein kinase ATP-binding motif

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Query Match 17.7%; Score 809.5; DB: 2; Length 825;
Best Local Similarity 26.1%; Pred. No. 2.2e-33;
Matches 252; Conservative 126; Mismatches 245; Indels 343; Gaps 36;
QY 6 NIPLVHI-----LTLVAFSGTEKL-----PKAPVITTPLETVDAIVEE 43
Db 79 NITSIHENMRSLLTNLAVDMLTYGLTKLSGLRSIQPRAPAKPHLYINLSNR 138
QY 44 VAFMCAVESYPOPEISWTNRKILKLPDTRYSIRENGQLTLISVED----- 91
Db 139 LTT-----LSM-----QLFQT-LSURE-----LQLEGNFNFGSCDIRMM 171

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QY 92 -----SDPGIYCCATNANGVGA-----VESGALQVYKKKIPTRPINVKI 132
Db 172 QLMQEGEALNLSNOLYCIAD-----GSQPLFRMINSQDL-----PEISVSHVLV 221
QY 133 IEGIKAVLPCTMGNPKPSVSWI-----KGDSPLENSRIAVLESGLRIHNVOKEDAG-Q 187
Db 222 REGDNNAVITCGSGPLPDVDWITVTGLQSIINTQNTNMTNVHAINLTIVNAVISEDGFT 281
QY 188 YRCVAKNSLG-----TAY--SKYVKLEFEVFAIRLRAPE--SHNVFGSFTVLC 234
Db 282 LFCIAENVVGMNSNAVALIYYPRVVSLE-----EPRLRLEHCIEF-----V 324
QY 235 ATGIPVPTIWIENGNAVSSGSI--QSVKRDYIDSLQLEFTRP-----GLYTCTATNK 287
Db 325 VRGNPPTLHMLNQGDLRSKTIHVEYQEGEISEGLLE-NKPTHYNGNNTLLAKNP 383
QY 288 HGEKFTAKAAATISTAEWSKPKQDNNGYCAQVRGEVCMNVLAKDALVELNTGSADEEA 347
Db 384 LG-----TANQITN-----GH-----FLKEPP--PEST 404
QY 348 QELLVHTAMNELKVSPVCPRAAEALCNHIFQECSPGVVPTPIPCREYCLAVELFCA 407
Db 405 DNFI-----LFDVSP----- 415
QY 408 KEWLMEKTHRGRLYRSEMILLVYKCSKLPKSHMDPTACARLPHLDYKNEKLTPEPMT 467
Db 416 -----TPPT 420
QY 468 -SSKPSVDIPPLPSSSSSFSVSPYSGMTVYISINSSFAIFVLTITLYCCRRRKQKN 526
Db 421 VTRKPEE-----TFGVSTAVGLAAACVLVLLVFMINKYGRSKFGM 464
QY 527 K-----KRESAAVT-----TLPSELLDLRLHPNM--YQRPDLLNKLISLEY 570
Db 465 KGPVAVISGEEDSASPLHINHGITPSSL--DAGPDYVAVIGMTRIPIVENPOYERQGN 521
QY 571 -----FRNNIEYVRDICEGAFGVFQARAGLLPYEPFTVAVKMLKEEASD 618
Db 522 NCHRPDTYYOHIKRDIKRLRELGEAGFVLAECYNLSPTKMKMLVAVKALKDPLLA- 580
QY 619 MQADFOREALMAEFDPNPIVTKLLGVAVKPMCLPEYMAVYGDLEFLRSMSPHTVCSL 678
Db 581 ARKDFOREALLTNLOHEHIYKFGYCGDDPLIMVEYKMGKDLNKLRAHGPN----- 635
QY 679 SHSDLSMRAQVSSPP-----PLSCAEQLCIARQVAAVAVLSERKFEVHRDLATRNCLV 733
Db 636 -----AMILVDGQPROAKGELGLSOMLHIASQIASGVYLAQHFEVHRDLATRNCLV 687
QY 734 GENNVYKIDPGLSRNITYSADYKANKENDAPIRMMPESIFYRNTTESDVNAVYGVV 793
Db 688 GANLLVYKIDPGLSRNITYSADYKANKENDAPIRMMPESIMRKFTTESDVNAVYGVV 747
QY 794 EIFSYGLQPYGYMAHEEVIYVRDGNILSCPEPCVELYNIMRCLMSKLPADRPSTSIH 853
Db 748 EIFTYKQPMFQSLNTEVEICITQGRVLEPRVCPKEVYDVLMQWREPOQLRIKEIY 807
QY 854 RILERM 859
Db 808 KILHAL 813

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RESULT 14

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JC4593
Protein-tyrosine kinase-related receptor PTK7 precursor - human
N:Alternate names: receptor protein tyrosine kinase-like protein (RPTK)
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
C:Accession: JC4593
R:Park, S.K.; Lee, H.S.; Lee, S.T.
J. Biochem. 119, 235-239, 1996
A:Title: Characterization of the human full-length PTK7 cDNA encoding a receptor prot
A:Reference number: JC4593; MUID:97037064
A:Accession: JC4593

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A: Molecule type: mRNA
A: Residues: 1-1070 <PAR>
C: Cross-references: GB:U04271; NID:91322231; PIDN:AAC0484.1; PID:91322232
C: Comment: This protein is a member of receptor protein tyrosine kinase family, but prot
C: Geneticks:
A: Gene: GDB:PTK7
A: Cross-references: GDB:134760; OMIM:601890
A: Map position: 6p21.1-6p12.2
C: Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C: Keywords: cell adhesion; extracellular protein; glycoprotein; phosphotransferase; tran
F: 1-30/Domain: signal sequence #status predicted <SIG>
F: 31-1070/Product: protein-tyrosine kinase 7 #status predicted <MAT>
F: 31-703/Domain: extracellular #status predicted <EXC>
F: 704-725/Domain: transmembrane #status predicted <TM>
F: 726-1070/Domain: intracellular #status predicted <INC>
F: 794-1065/Domain: protein kinase homology <KIN>
F: 116,175,184,214,268,283,405,463,567,646/Binding site: carbohydrate (Asn) (covalent) #

Query Match 17.4%; Score 793; DB 2; Length 1070;
Best Local Similarity 27.8%; Pred. No. 1.9e-32;
Matches 233; Conservative 136; Mismatches 300; Indels 168; Gaps 30;

QY 55 POPELSMTNRKILIKLPDTRYSIRENGQLTILSVSDSDGICYCTANNCGAVESGCA 114
DB 350 PEPSSVMEHAGVRL--PTGHRVYQKGHELVLANIAESDAGVYTCHAAANLAQORQDVN- 405
QY 115 LQVKKPKITRPPINVKIIEGLKAVLPCTMGNPKPSYMWIGSDSPRLRENSRIAVLESQS 174
DB 406 ITVAIVPSPMIAKKRPODSOLEGKPGYLDLTQATPKPTVYWRNOMLISDSFEYFKNGT 465
QY 175 LRINVOKEDEAGQYRCVAKNSLGT--AVSKVYKLEFEVFAIRLAPESHN-VTFGSEVYL 231
DB 466 LRINSVEYEDGTWYRCMSSTPAGSIEAQRVYLEKFT--PPQPOQCEFEFKKATV 522
QY 232 HCTAGIVPPTITWENGNVSSGSIQSVKDRVIDSRLOLEFTR-----POLYICITATN 286
DB 523 PCSATGRKRPITTKWR-----ADGS--SLPEWVDNMGTLFAVNTDDAGNYICIASN 574
QY 287 KHGEFTAKAAATISIAEWSKPKDNKGYCAQYRGECVNAVLAKDALVFLNTSYADPEE 346
DB 575 -----GPGQIRAHVQLVY-----AVFI-TFKEVERP 600
QY 347 AOELLVHTANMELKLVSPYCPRAEALLCNHIFQCSGCVVPTPIPIREYCLAVKELFC 406
DB 601 TTVYQGHFA-----LLOCEAOGDPKPL----- 622
QY 407 AKEWLVMEKTRHGLYRSEHMLSVKCSKLPMSH-----WDPICARLPHTDY 455
DB 623 -IQW-----KKDKILDPITLG--PRMHIFQNGSLVHDVAPEDSGRTTCIAG 667
QY 456 NKEMLK-TFPPMTSSKPSVDIPNLPSSSSSSFVSPTYSM--TVIISIMSSFALVLLTI 512
DB 668 NSCHIKHTEAPLY---VVDKP-VPSESECPGS-PPPYKMIQTIGLSGAAVAIVIAVLG 721
QY 513 TTLVC-----CRRRQWKNNKRESAAVTL-----TLLPSLLDLRLHPNMYRM 557
DB 722 LMFCKCKRCKKRILOKOREGEPEMECLNGPRLONGOPASBIOEVALTISGSGAATNK 781
QY 558 PLLNPKLLSEYRNNIEYVRDIEGAFGRVFOARAGLLPYEFPTVAVKMLKEESA 617
DB 782 RHSTSDK---MHPRSSIOPITTLGKSEFGVFLAKAGLEGAETLVLKSLQTK-DE 837
QY 618 DMQADFOREALMAEFQNPNIYKLLGCYAVGKPKCLFEYVAGDNLNFEFLSMSPHYCS 677
DB 838 QOQDLDFRELEMGKLNIAVYRLLGLCREAPHYMYLEVYDLDLKQFLR----- 888
QY 678 LSHS-DLSMAQVSSPPPLSCAEOLCIAROVAGMAVYSEKRVHDLTRNCTIYGEN 736
DB 889 ISKSKDEKLKQ-----PLSTKQKVALCTQVALGHEHLSNNRPFVKDLARAKCLVSAQ 941
QY 737 MVYKIDPGLSRLNITYSADYKANKENDAIPIRMMPESITFYRNYTESDVNAVGVLEIF 796
DB 796 ----- 1000

DB 942 ROVKVYALGLSKDYNSSEYHFERO-AWVPLRWMSPAILLEGDFSTKSDVWAFGLMMEYF 1000
QY 797 SYGLQPYQYMAHEVITYYRRDGNH-LSCPEKNCPEVELYNLMRCWKSLLPADRPSFTSI 852
DB 1001 THEEMPHGOADDEVLIADLQAGAKARLPQPEGCPSKLYRLMORCMWALSPKDRPSFEI 1057

RESULT 15
173632
neurotrophin-3 receptor precursor - human
N: Alternate names: receptor tyrosine kinase trkC
N: Contains: protein-tyrosine kinase (EC 2.7.1.112)
C: Species: Homo sapiens (man)
C: Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jun-1999
C: Accession: 173632
R: Shetton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.
J. Neurosci. 15, 477-491, 1995
A: Title: Human trks: molecular cloning, tissue distribution, and expression of extrac
A: Reference number: 156557; MUID:95123473
A: Accession: 173632
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-839 <RES>
A: Cross-references: GB:S76475; NID:9913721; PIDN:AAB33111.1; PID:9913722
C: Geneticks:
A: Gene: GDB:NTRK3; TRKC
A: Cross-references: GDB:127899; OMIM:191316
A: Map position: 15q24-15q25
C: Function:
A: Description: regulation of nervous system development; receptor for neurotrophin-3
C: Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc
C: Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; ph
F: 1-31/Domain: signal sequence #status predicted <SIG>
F: 32-839/Product: neurotrophin-3 receptor #status predicted <MAT>
F: 32-436/Domain: extracellular #status predicted <EXC>
F: 79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F: 104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F: 128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F: 151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F: 437-839/Domain: transmembrane #status predicted <TM>
F: 454-839/Domain: cytosolic #status predicted <CYT>
F: 536-831/Domain: protein kinase homology <KIN>
F: 546-552/Region: protein kinase ATP-binding motif
F: 72,79,133,163,203,218,232,259,267,294,375,388/Binding site: carbohydrate (Asn)
F: 572/Active site: Lys #status predicted
F: 709/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi
F: 834/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 17.3%; Score 792.5; DB 1; Length 839;
Best Local Similarity 25.9%; Pred. No. 1.6e-32;
Matches 254; Conservative 125; Mismatches 244; Indels 357; Gaps 38;

QY 6 NIPLVHT-----LTLVAFSGTEKL-----PKAVITPTLETVALYEE 43
DB 79 NITSIHENMNSLMTLANVDMELTYGLQKLTIKNSGLNSIOPRAAKNPHRYINLSSNR 138
QY 44 VATEMCAYESYPOPEISWTRNKKILIKLPDTRYSIRENGQLTILSVED----- 91
DB 139 LTT-----LSN-----QLFQT-LSLRE-----LQLEONFENGSCDIRM 171
QY 92 -----SDGICYCTANNVGA-----VESCGLQVKKPKITRPPINVKI 132
DB 172 QLMQDGEAKLNQNLXICIND---GSQLPLFRNNIQCDL-----PEISVSHVNTLV 221
QY 133 IEGKAVLPCTTMGNPKPSYMI-----KGDSPLRNSRIAVLESGLRIHVQKQDAG-Q 187
DB 222 REGDNAVITTCNGSGSPPLDVMTYITGLQSTINRQTNLMWTVAHINTLVVNTSDDNFT 281
QY 188 YRCVAKNSLG-----TAY--SKVYKLEFEVFAIRLAPD-----SHNVTFGSEFVTLHCT 234
DB 282 LTCIAENVVGNASVALTYYVPRVSL-----EPRLRLEHIEF-----V 324

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2002, 13:36:00 ; Search time 37.92 Seconds

(without alignments)
3964.467 Million cell updates/sec

Title: US-09-817-487a-2

Perfect score: 4569

Sequence: 1 MRELVINIPVHILTLVAFSG.....TSIHRILERMOCERAGTGVSV 869

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4558	99.8	869	4	015146
2	4282.5	93.9	868	11	062838
3	4269.5	93.4	868	11	061006
4	4220.5	92.4	860	11	061005
5	4136	90.5	871	11	061987
6	4128	90.3	881	11	061988
7	2897	63.4	946	13	007153
8	1602	33.1	354	13	007153
9	1129.5	24.7	724	5	09V6K3
10	966.5	21.2	1145	5	09V6K3
11	802	17.6	821	13	09YH44
12	801	17.5	811	13	09YH43
13	792.5	17.3	839	4	075682
14	778	17.0	865	5	024488
15	773.5	16.9	928	5	09BLV1
16	772	16.9	902	5	017576

17	754.5	16.5	591	4	015656	015656 homo sapien
18	750.5	16.4	790	13	090699	090699 gallus gall
19	740.5	16.2	503	4	015655	015655 homo sapien
20	738.5	16.2	486	13	09PST9	09PST9 xenopus lae
21	724.5	15.9	802	13	042127	042127 xenopus lae
22	720	15.8	782	11	061563	061563 mus musculu
23	720	15.8	796	13	021287	021287 pleurodeles
24	720	15.8	972	5	026614	026614 strongyloce
25	715	15.6	800	4	099052	099052 homo sapien
26	712	15.6	282	13	091373	091373 xenopus. tr
27	709	15.5	800	11	09JHX9	09JHX9 rattus norv
28	708	15.5	922	13	090413	090413 brachydanio
29	705.5	15.4	814	13	091887	091887 xenopus lae
30	702.5	15.4	802	6	095M13	095M13 bos taurus
31	697.5	15.3	650	11	063709	063709 rattus rat
32	696.5	15.2	810	13	09P596	09P596 xenopus lae
33	695.5	15.2	800	13	0918X3	0918X3 brachydanio
34	690.5	15.1	989	13	09PMW6	09PMW6 gallus gall
35	686.5	15.0	824	13	090749	090749 gallus gall
36	681	14.9	766	4	096KM2	096KM2 homo sapien
37	681	14.9	785	4	096KM1	096KM1 homo sapien
38	681	14.9	819	4	096KM0	096KM0 homo sapien
39	679	14.9	822	11	060818	060818 mus musculu
40	677	14.8	876	11	060752	060752 mus musculu
41	676	14.8	782	6	09RT23	09RT23 oryctolagus
42	676	14.8	806	13	090Z00	090Z00 brachydanio
43	671	14.7	609	13	091776	091776 xenopus lae
44	670	14.7	1358	13	073798	073798 xenopus lae
45	670	14.7	1362	13	09PV24	09PV24 xenopus lae

ALIGNMENTS

RESULT 1
ID 015146 PRELIMINARY: PRT: 869 AA.
AC 015146;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MUSCLE SPECIFIC TYROSINE KINASE RECEPTOR.
GN MUSK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009854; PubMed=7546737;
RA Valenzuela D.M., Stitt T.N., Distefano P.S., Rojas E., Mattsson K.,
RA Compton D.L., Nunez L., Park J.S., Stark J.L., Giles D.R., Thomas S.,
RA Lebeau M.M., Fernald A.A., Copeland N.G., Jenkins N.A., Buden S.J.,
RA Glass D.D., Yancopoulos G.D.;
RT "Receptor tyrosine kinase specific for the skeletal muscle lineage:
RT expression in embryonic muscle, at the neuromuscular junction, and
RT after injury.";
RT Neuron 15:573-584(1995).
[2]
SEQUENCE FROM N.A.
RA Valenzuela D.M., Rojas E., Yancopoulos G.D.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF006464; AAB63044.1; -;
DR HSSP: P11362; IFGK.
DR InterPro: IPR002453; Beta.tubulin.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF01047; Ig; 3.
DR Pfam: PF00069; pkinase; 1.

PRINTS: PRO0109; TYRKINASE.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00038; FZ; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
 DR ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
 KW Tyrosine-protein kinase.
 SO SEQUENCE 869 AA; 97056 MW; 3DDC20E179FA010C CRC64;

Query Match 99.8%; Score 4558; DB 4; Length 869;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MRELVINPIVLHILTLVAFSGTEKLPKAPVITTPLETVDALEEVATFMCVAVESYPOPEIS 60
DB 1 MRELVINPIVLHILTLVAFSGTEKLPKAPVITTPLETVDALEEVATFMCVAVESYPOPEIS 60
Y 61 WTRNKILIKLFDTRYSTRIRNGQLTTLISVEDSDGIYCCCTANNVGAVESCGALQYKMK 120
DB 61 WTRNKILIKLFDTRYSTRIRNGQLTTLISVEDSDGIYCCCTANNVGAVESCGALQYKMK 120
QY 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSMIKGDSPLREMSRIAVLESGLRIHNV 180
DB 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSMIKGDSPLREMSRIAVLESGLRIHNV 180
QY 181 OKEDAGQRCYVAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSFVTLHCTATGIPV 240
DB 181 OKEDAGQRCYVAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSFVTLHCTATGIPV 240
QY 241 PPTIWIINGNAVSSGSIOESVKDVIDSRLOLFTFKPGLTCTATNKGHEKSTAKAAAT 300
DB 241 PPTIWIINGNAVSSGSIOESVKDVIDSRLOLFTFKPGLTCTATNKGHEKSTAKAAAT 300
QY 301 ISIAEMSKPOKDNKGCAQYRGECVNAVLAKDALVFLNTSYADEEAOELLVHTAMNELK 360
DB 301 ISIAEMSKPOKDNKGCAQYRGECVNAVLAKDALVFLNTSYADEEAOELLVHTAMNELK 360
QY 361 VVSVCPAPAAALCNHIFOECSGCVPTPTPTICRECLAVKELFCAKEMLYMEKTHRG 420
DB 361 VVSVCPAPAAALCNHIFOECSGCVPTPTPTICRECLAVKELFCAKEMLYMEKTHRG 420
QY 421 LYREEMHLSPKCSKLPMSHMDPTACARPLHDYKNENKTFPPMSSSKSVDIPLNLS 480
DB 421 LYREEMHLSPKCSKLPMSHMDPTACARPLHDYKNENKTFPPMSSSKSVDIPLNLS 480
QY 481 SSSSSFSVSPYTSMTVIISIMSSFAIFVLLTTTLYCCRRKKQKMKKRESAAVTLTLP 540
DB 481 SSSSSFSVSPYTSMTVIISIMSSFAIFVLLTTTLYCCRRKKQKMKKRESAAVTLTLP 540
QY 541 SELLDRLHPPMPQORPMLLPKLLSLSEYPRNNIEYVROIGEGAFGVPPARAPGLLPY 600
DB 541 SELLDRLHPPMPQORPMLLPKLLSLSEYPRNNIEYVROIGEGAFGVPPARAPGLLPY 600
QY 601 EPTFMVAVKMLKEBASADMDQFORAALMAEFDPNPVILKLGCAVAGKPCMLTFEYVAY 660
DB 601 EPTFMVAVKMLKEBASADMDQFORAALMAEFDPNPVILKLGCAVAGKPCMLTFEYVAY 660
QY 661 GDLNEFLKMSPHTVCSLISHSDLSMRAOVSSPPPLSCAEOLCIAROVAAGMAYLSERK 720
DB 661 GDLNEFLKMSPHTVCSLISHSDLSMRAOVSSPPPLSCAEOLCIAROVAAGMAYLSERK 720
QY 721 FVHBDLATRNCLVGENMYVKTADFGSLSNITYSADYKANKENDALPIRMPPESTIFYNYT 780
DB 721 FVHBDLATRNCLVGENMYVKTADFGSLSNITYSADYKANKENDALPIRMPPESTIFYNYT 780
QY 781 TESDVAAGVVLMEIFSGIOPYYGMAHEEVIYYVROGNIISCPENCPEVELYNLMRLCWS 840
DB 781 TESDVAAGVVLMEIFSGIOPYYGMAHEEVIYYVROGNIISCPENCPEVELYNLMRLCWS 840

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QY 841 KLPADRPSTSIHRLIEMRCERAEGTVSV 869
 DB 841 KLPADRPSTSIHRLIEMRCERAEGTVSV 869

RESULT 2
 ID 062838 PRELIMINARY; PRT; 868 AA.
 AC 062838;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE MUSCLE-SPECIFIC TYROSINE KINASE RECEPTOR M05K.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96009854; PubMed=7546737;
 RA Valenzuela D.M., Stilt T.N., Distefano P.S., Rojas E., Mattsson K.,
 RA Compton D.L., Nunez L., Park J.S., Stark J.L., Gies D.R., Thomas S.,
 RA LeBeau M.M., Fernald A.A., Copeland N.G., Jenkins N.A., Burden S.J.,
 RA Glass D.J., Yancopoulos G.D.;
 RT "Receptor tyrosine kinase specific for the skeletal muscle lineage:
 RT expression in embryonic muscle, at the neuromuscular junction, and
 RT after injury.";
 RL Neuron 15:573-584(1995).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: U34985; AAA0956.1; -.
 DR HSSP: P11362; 1EGK
 DR InterPro: IPR002453; Beta_tubulin.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PRO0109; TYRKINASE.
 DR SMART: SM00408; IGC2; 3.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00038; FZ; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
 KW ATP-binding; Immunoglobulin domain; Kinase; Receptor;
 KW Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 868 AA; 96821 MW; C146B4E74EE25B24 CRC64;

Query Match 93.9%; Score 4292.5; DB 11; Length 868;
 Best Local Similarity 93.2%; Pred. No. 0;
 Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

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QY 1 MRELVINPIVLHILTLVAFSGTEKLPKAPVITTPLETVDALEEVATFMCVAVESYPOPEIS 60
DB 1 MRELVINPIVLHILTLVAFSGTEKLPKAPVITTPLETVDALEEVATFMCVAVESYPOPEIS 60
QY 61 WTRNKILIKLFDTRYSTRIRNGQLTTLISVEDSDGIYCCCTANNVGAVESCGALQYKMK 120
DB 61 WTRNKILIKLFDTRYSTRIRNGQLTTLISVEDSDGIYCCCTANNVGAVESCGALQYKMK 120
QY 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSMIKGDSPLREMSRIAVLESGLRIHNV 180
DB 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSMIKGDSPLREMSRIAVLESGLRIHNV 180
QY 181 OKEDAGQRCYVAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSFVTLHCTATGIPV 240
DB 181 OKEDAGQRCYVAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSFVTLHCTATGIPV 240

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Db 181 QKEDAGQYRCVAKNSLGTAYSKLVKLEVEFARILRAPESHNTFGSEVTLRCTAIGMPV 240
QY 241 PTTIWIENGNAVSSGSIQSVKDRVIDSRLOLFTPKGLYTCTATNKHGEKSTAKAAAT 300
Db 241 PTTIWIENGNAVSSGSIQSVKDRVIDSRLOLFTPKGLYTCTATNKHGEKSTAKAAAT 300
QY 301 ISIAEWSKQKDNKGCAQYRGEVCNAVLAKDALVFLNTSYADPEBAQELLVHTANNEK 360
Db 301 ISIAEWSKQKDNKGCAQYRGEVCNAVLAKDALVFLNTSYADPEBAQELLVHTANNEK 360
QY 361 VSPVCRPAEAALLCNHIEQESPGVPTPIPCREYCLAVKELFCAKELVMEETHNG 420
Db 361 VSPVCRPAEAALLCNHIEQESPGVPTPIPCREYCLAVKELFCAKELVMEETHNG 420
QY 421 LYRSEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEKLTFFPMTSSKPSVDINLPS 480
Db 421 LYRSGNHFLPYRPECSTLPSMHDPTACTRLPYLDYKKEITTFPTSSKPSVDINLP- 479
QY 481 SSSSSFSVSPYVSMVYIISIMSSFAIFVLLTTTLYCCRRRQWKKKRESAAVLTTLTP 540
Db 480 ASTSSFAVSPAYSMVYIISIMSCFAVFAVLLTTTLYCCRRREMKKKRESAAVLTTLTP 539
QY 541 SELLDRLHPNMYOMRPLLNPKLLSTLEYPRNNIEYVNDIGEGARGVFOARAPGLPY 600
Db 540 SELLDRLHPNMYOMRPLLNPKLLSTLEYPRNNIEYVNDIGEGARGVFOARAPGLPY 599
QY 601 EPTTVAVAMKLEASADQADFOREAAALMAEFDNPNIKYLCVCAVGGKPMCLFFETMAY 660
Db 600 EPTTVAVAMKLEASADQADFOREAAALMAEFDNPNIKYLCVCAVGGKPMCLFFETMAY 659
QY 661 GDLNEFLKSMSPHTVCSLSHSDLSMRQVSSGPPPLSCAEQDCLARQVAAAGMAYLSERK 720
Db 660 GDLNEFLKSMSPHTVCSLSHSDLSMRQVSSGPPPLSCAEQDCLARQVAAAGMAYLSERK 719
QY 721 FVHRDLATRNCLVGENMVKYIADFGLSRNIYSADYKKAENOAIPTRMMPPEISFYNNRT 780
Db 720 FVHRDLATRNCLVGENMVKYIADFGLSRNIYSADYKKAENOAIPTRMMPPEISFYNNRT 779
QY 781 TESDVAYGVVLMEIFSYGLQPYGYMAHEVITYYVADGNILSCPENCPVELYNLMKLS 840
Db 780 TESDVAYGVVLMEIFSYGLQPYGYMAHEVITYYVADGNILACPEKCPLELYNLMKLS 839
QY 841 KLPADRPSTSTHRLIERMCCERAGEVSY 869
Db 840 KLPADRPSTSTHRLIERMCCERAGEVSY 868

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RESULT 3

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ID 061006 PRELIMINARY: PRT: 868 AA.
AC 061006:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MUSCLE LOCALIZED KINASE 2.
OS Mus musculus (Mouse).
OC Euteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Caruso A., Morris J.C., Neben S., Flinerty H., Belter D., Turner K.,
RA Wood C.R.;
RL Submitted (OCT-1995) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U37709; AAA79204.1; -.
DR HSSP: P11362; IFGK
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Iq_c2.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR002290; Ser_thr_kinase.

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DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF01392; Fz_1.
DR Pfam: PF00047; Iq_3.
DR Pfam: PF00069; pkinase_1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGC2_3.
DR SMART: SM00219; TYRK_1.
DR PROSITE: PS00308; Fz_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS50018; PROTEIN_KINASE_DOM_1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE: PS00228; TUBULIN_B_AUTOREG_1.
KW ATP-binding; Immunoglobulin domain; Kinase;
KW Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 868 AA; 96692 MW; AFE4E644C6869933 CRC64;

Query Match 93.4%; Score 4269.5; DB 11; Length 868;
Best local similarity 92.9%; Pred. No. 0;
Matches 807; Conservative 30; Mismatches 31; Indels 1; Gaps 1;

QY 1 MRELVIPLVHLITLVAFGSTKLPKAPVITTPLETVDALVEVATPMCAVESYPOPEIS 60
Db 1 MRELVINIPLQMLTLVAFSGTEKLPKAPVITTPLETVDALVEVATPMCAVESYPOPEIS 60
QY 61 WTRNKLLILFDTRYISIRENGQLTLTVSDSDGTYCCANNGVGGAVESGALGVKK 120
Db 61 WTRNKLLILFDTRYISIRENGQLTLTVSDSDGTYCCANNGVGGAVESGALGVKK 120
QY 121 PKTRPPINVKITIEGLKAVLPCTTMGNPKPSVSMKIGDSPLENSRIAVLESGSLRIHNV 180
Db 121 PKTRPPINVKITIEGLKAVLPCTTMGNPKPSVSMKIGDNALRENSRIAVLESGSLRIHNV 180
QY 181 QKEDAGQYRCVAKNSLGTAYSKLVKLEVEFARILRAPESHNTFGSEVTLRCTAIGIPV 240
Db 181 QKEDAGQYRCVAKNSLGTAYSKLVKLEVEFARILRAPESHNTFGSEVTLRCTAIGIPV 240
QY 241 PTTIWIENGNAVSSGSIQSVKDRVIDSRLOLFTPKGLYTCTATNKHGEKSTAKAAAT 300
Db 241 PTTIWIENGNAVSSGSIQSVKDRVIDSRLOLFTPKGLYTCTATNKHGEKSTAKAAAT 300
QY 301 ISIAEWSKQKDNKGCAQYRGEVCNAVLAKDALVFLNTSYADPEBAQELLVHTANNEK 360
Db 301 ISIAEWSKQKDNKGCAQYRGEVCNAVLAKDALVFLNTSYADPEBAQELLVHTANNEK 360
QY 361 VSPVCRPAEAALLCNHIEQESPGVPTPIPCREYCLAVKELFCAKELVMEETHNG 420
Db 361 VSPVCRPAEAALLCNHIEQESPGVPTPIPCREYCLAVKELFCAKELVMEETHNG 420
QY 421 LYRSEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEKLTFFPMTSSKPSVDINLPS 480
Db 421 LYRSEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEKLTFFPMTSSKPSVDINLPS 480
QY 480 ASTSSFAVSPAYSMVYIISIMSSFAIFVLLTTTLYCCRRRQWKKKRESAAVLTTLTP 539
Db 480 ASTSSFAVSPAYSMVYIISIMSSFAIFVLLTTTLYCCRRRQWKKKRESAAVLTTLTP 539
QY 541 SELLDRLHPNMYOMRPLLNPKLLSTLEYPRNNIEYVNDIGEGARGVFOARAPGLPY 600
Db 540 SELLDRLHPNMYOMRPLLNPKLLSTLEYPRNNIEYVNDIGEGARGVFOARAPGLPY 599
QY 601 EPTTVAVAMKLEASADQADFOREAAALMAEFDNPNIKYLCVCAVGGKPMCLFFETMAY 660
Db 600 EPTTVAVAMKLEASADQADFOREAAALMAEFDNPNIKYLCVCAVGGKPMCLFFETMAY 659
QY 661 GDLNEFLKSMSPHTVCSLSHSDLSMRQVSSGPPPLSCAEQDCLARQVAAAGMAYLSERK 720
Db 660 GDLNEFLKSMSPHTVCSLSHSDLSMRQVSSGPPPLSCAEQDCLARQVAAAGMAYLSERK 719
QY 721 FVHRDLATRNCLVGENMVKYIADFGLSRNIYSADYKKAENOAIPTRMMPPEISFYNNRT 780
Db 720 FVHRDLATRNCLVGENMVKYIADFGLSRNIYSADYKKAENOAIPTRMMPPEISFYNNRT 779

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QY 781 TESDVMAVGVLMWEIFSYGLQPYGMAHEEYIYVRDGNILSCPCNPVELYINMLRCLWS 840
DB 780 TESDVMAVGVLMWEIFSYGLQPYGMAHEEYIYVRDGNILSCPCNPVELYINMLRCLWS 839
QY 841 KLPADRPFSFHSIRHILERMCEAEGTVSV 869
DB 840 KLPADRPFSFHSIRHILERMCEAEGTVGV 868

RESULT 4
ID 061005 PRELIMINARY; PRT; 860 AA.
AC 061005;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MUSCLE LOCALIZED KINASE 1.
GN MK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Caruso A., Morris J.C., Neben S., Finnerty H., Beier D., Turner K.,
RA Wood C.R.;
RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U37708; AAA79203.1; -.
DR HSSP: P11362; IFGK.
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF01392; Fz_1.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF00069; pkinase_1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00219; TYRKc_1.
DR PROSITE: PS50038; FZ; 1.
DR PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
DR ATP-binding: Immunoglobulin domain; Kinase; Transferase;
KW Tyrosine-protein kinase.
KW SEQUENCE 860 AA; 95670 MW; A837F8299BD7494C CRC64;
2

Query Match 92.4%; Score 4220.5; DB 11; Length 860;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 801; Conservative 29; Mismatches 30; Indels 9; Gaps 2;

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DB 241 PTIWIENGNAVSSGSIOESVKDVRIDSRLOLFTTKGGLYCIATNNHGEFSTAKAAT 300
QY 301 ISIIEWSPKDNKGCAOYAGEVCNNAVLAKDALVPLNTSVADDEAOELLVHTANNEK 360
DB 301 ISIIEWSPKDNKGCAOYAGEVCNNAVLAKDALVPLNTSVADDEAOELLVHTANNEK 360
QY 361 VSPVCRPAEALLCNHIFQCSGPGVVPPIPIGREYCLAVKELFCAKEWLMEEKTHRG 420
DB 361 AVSPLCRPAEALLCNHIFQCSGPGVVPPIPIGREYCLAVKELFCAKEWLMEEKTHRG 420
QY 421 LYRSEMHLLSPKCSKLPMSHMDPTACARLPHLDYNNENLTPPMNLSKRSVDLPILPS 480
DB 421 LYRSGMHLLPYECSKLPMSHMDPTACTRPLYL-----AFPSITSSRSADIPNL 471
QY 481 SSSSFSPSPMTVIISIMSFATFVLTITTLTYCCRRRQKMKKRESAATLTPLP 540
DB 472 ASISFSPSPMTVIISIMSFATFVLTITTLTYCCRRRQKMKKRESTATLTPLP 531
QY 541 SELLDRLHPNMQRMPLLNPLLSLEYPRNNIEYVRDIGEGAFGRVQARAPGLLPY 600
DB 532 SELLDRLHPNMQRMPLLNPLLSLEYPRNNIEYVRDIGEGAFGRVQARAPGLLPY 591
QY 601 EPTFMVAVKMLKEBASADMQADFORBAALAEFDPNPVYLLGYCAVCKPKCLLFYVAY 660
DB 592 EPTFMVAVKMLKEBASADMQADFORBAALAEFDPNPVYLLGYCAVCKPKCLLFYVAY 651
QY 661 GDNLNPLKSMSPHTVCSLHSDLSMRAOVSPGPPPLSCAQOLCIAROVAAGMAYLSERK 720
DB 652 GDNLNPLKSMSPHTVCSLHSDLSMRAOVSPGPPPLSCAQOLCIAROVAAGMAYLSERK 711
QY 721 FVHRDLATRNCLVGENNVYKIADEGLSRNYSADYKANENDAIPIRMPPESIFYNRY 780
DB 712 FVHRDLATRNCLVGENNVYKIADEGLSRNYSADYKANENDAIPIRMPPESIFYNRY 771
QY 781 TESDVMAVGVLMWEIFSYGLQPYGMAHEEYIYVRDGNILSCPCNPVELYINMLRCLWS 840
DB 772 TESDVMAVGVLMWEIFSYGLQPYGMAHEEYIYVRDGNILSCPCNPVELYINMLRCLWS 831
QY 841 KLPADRPFSFHSIRHILERMCEAEGTVSV 869
DB 832 KLPADRPFSFHSIRHILERMCEAEGTVGV 860

RESULT 5
ID 061987 PRELIMINARY; PRT; 871 AA.
AC 061987;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NSK2 PROTEIN PRECURSOR.
DE MUSK OR NSK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-myoblast;
RC MEDLINE=95349951; PubMed=7624144;
RX Ganju P., Walls E., Brennan J., Reich A.D.;
RT "Cloning and developmental expression of Nsk2, a novel receptor
RT tyrosine kinase implicated in skeletal myogenesis...";
RL OncoGene 11:281-290(1995).
CC -1- SIMILARITY: BELONGS TO THE SPR/THR FAMILY OF PROTEIN KINASES.
DR EMBL: X86444; CAA60165.1; -.
DR HSSP: P11362; IFGK.
DR MGD: MGI:103581; Musk.
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Ig_c2.

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DR InterPro: IPR003600; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00069; kinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00410; IG-like; 1.
 DR SMART: SM00219; TyKc; 1.
 DR PROSITE: PS50038; Fz; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
 DR ATP-binding; Immunoglobulin domain; Serine/threonine-protein kinase;
 KW Signal; Transferase.
 FT SIGNAL 1
 SQ SEQUENCE 871 AA; 97047 MW; F3C53DC6AFE702AB CRC64;

Query Match 90.5%; Score 4136; DB 11; Length 871;

Best Local Similarity 90.3%; Pred. No. 0;

Matches 790; Conservative 30; Mismatches 45; Indels 10; Gaps 4;

OY 1 MRELVINPVLHITLVAFGSTETKLPKAPVITTPLETVDAIVEVATFMCVESTPOPEIS 60
 DB 1 MRELVINPVLHITLVAFGSTETKLPKAPVITTPLETVDAIVEVATFMCVESTPOPEIS 60
 OY 61 WTRNKLILKLPDTRYSIRENGQLLTLLSYEDSDGICYCTANNGVGAVERSCALGVKMK 120
 DB 61 WTRNKLILKLPDTRYSIRENGQLLTLLSYEDSDGICYCTANNGVGAVERSCALGVKMK 120
 OY 61 WTRNKLILKLPDTRYSIRENGQLLTLLSYEDSDGICYCTANNGVGAVERSCALGVKMK 120
 DB 61 WTRNKLILKLPDTRYSIRENGQLLTLLSYEDSDGICYCTANNGVGAVERSCALGVKMK 120
 OY 121 PRTTRPPIVVKITIEGKAVLPCTTKGNPKPSVWIKGDSPLRENSKRAVESSSLKHNV 180
 DB 121 PRTTRPPIVVKITIEGKAVLPCTTKGNPKPSVWIKGDSPLRENSKRAVESSSLKHNV 180
 OY 181 OKEDAGQYRCVAKNSLGTYSKVVKLEFEYFARILRAPESHNTFCSFVTLHGTATGIPV 240
 DB 181 OKEDAGQYRCVAKNSLGTYSKVVKLEFEYFARILRAPESHNTFCSFVTLHGTATGIPV 240
 OY 241 PRTTWIENGNAVSSGSIQESVKDVIDSRQLQETFRPGLYTCIATNKGKESFSTAAAT 300
 DB 241 PRTTWIENGNAVSSGSIQESVKDVIDSRQLQETFRPGLYTCIATNKGKESFSTAAAT 300
 OY 301 ISTAEMSKQOKNKGYCAQYRGVCNAVL-----AKDALVEL-NTSYADPEEQELLVHT 354
 DB 301 ISTAEMSKQOKNKGYCAQYRGVCNAVL-----AKDALVEL-NTSYADPEEQELLVHT 354
 OY 355 ANNELKVPVPCRAEALCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEMLVME 414
 DB 355 ANNELKVPVPCRAEALCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEMLVME 414
 OY 415 EYTHRGVLYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYKNEKLTTPPMPTSSKPSVD 474
 DB 415 EYTHRGVLYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYKNEKLTTPPMPTSSKPSVD 474
 OY 478 ITPLPSSSSSPSVPTTYMTVITISMSFAITVLTITTLTYCCRRKQKNNKRESAAV 534
 DB 478 ITPLPSSSSSPSVPTTYMTVITISMSFAITVLTITTLTYCCRRKQKNNKRESAAV 534
 OY 535 TLTTPSELLDLRHPNPMYORPMLLPNKLISLEYPRNNIEYVRIDIGEGAFRVOARA 594
 DB 535 TLTTPSELLDLRHPNPMYORPMLLPNKLISLEYPRNNIEYVRIDIGEGAFRVOARA 594
 OY 597 PGLLPYEPPTMAVVKMLKEEASADMQADFQREAAALMAEFDNPNIVKLGVCAVGKPMCLL 654
 DB 597 PGLLPYEPPTMAVVKMLKEEASADMQADFQREAAALMAEFDNPNIVKLGVCAVGKPMCLL 654
 OY 655 FEYMAVGDLNEFLRSMSPHTVCSLSHSDLSMRQVSSPGPPPLSCAEOQLCIARQVAAGMA 714
 DB 655 FEYMAVGDLNEFLRSMSPHTVCSLSHSDLSMRQVSSPGPPPLSCAEOQLCIARQVAAGMA 714

DB 657 FEYMAVGDLNEFLRSMSPHTVCSLSHSDLSSTRARVSSPGPPPLSCAEOQLCIARQVAAGMA 716
 OY 715 YLSERKFVHRDLAPRNCVGENNVVKIADFGLSRNTIYSADYKYKANENDALPIRMPEST 774
 DB 717 YLSERKFVHRDLAPRNCVGENNVVKIADFGLSRNTIYSADYKYKANENDALPIRMPEST 776
 OY 775 FYNRRTESDVMAYGVVLMWEIFSYGLOPYGMAHEEYIYVRDGNILSCPNCPELVLYNL 834
 DB 777 FYNRRTESDVMAYGVVLMWEIFSYGLOPYGMAHEEYIYVRDGNILSCPNCPELVLYNL 836
 OY 835 MRLCWSKLPADRPSTSIHRIERMCERAGTVSV 869
 DB 837 MRLCWSKLPADRPSTSIHRIERMCERAGTVSV 871

RESULT 6

ID 061988 PRELIMINARY; PRT; 881 AA.
 AC 061988;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NSK2 PROTEIN PRECURSOR.
 GN MUSK OR NSK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MYOBLAST;
 RX MEDLINE=95349951; PubMed=7624144;
 RA Ganju P., Walls E., Brennan J., Reith A.D.;
 RT "Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase implicated in skeletal myogenesis,";
 RT Oncogene 11:281-290(1995).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: X86445; CAA60166.1; -.
 DR HSSP: P11362; IFGK.
 DR MGD: MGI:103581; MusK.
 DR InterPro: IPR002453; Beta_tubulin.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig_like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00069; kinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00410; IG-like; 1.
 DR SMART: SM00219; TyKc; 1.
 DR PROSITE: PS50038; Fz; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
 DR ATP-binding; Immunoglobulin domain; Serine/threonine-protein kinase;
 KW Signal; Transferase.
 FT SIGNAL 1
 SQ SEQUENCE 881 AA; 98435 MW; EA0D0282E9828ED7 CRC64;

Query Match 90.3%; Score 4128; DB 11; Length 881;

Best Local Similarity 90.4%; Pred. No. 0;

Matches 788; Conservative 30; Mismatches 44; Indels 10; Gaps 4;

OY 1 MRELVINPVLHITLVAFGSTETKLPKAPVITTPLETVDAIVEVATFMCVESTPOPEIS 60
 DB 1 MRELVINPVLHITLVAFGSTETKLPKAPVITTPLETVDAIVEVATFMCVESTPOPEIS 60

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Db 1 MRELVINPILLOMLTLVAESGTEKLPKPPVIATPLETVDAIVEEATWCAVESYPOPEIS 60
QY 61 WTRKILIKLEFDTYSIRENGQLITLISVEDSDGIVCCPTANNNGVGVESGALQVKKM 120
Db 61 WTRKILIKLEFDTYSIRENGQLITLISVEDSDGIVCCPTANNNGVGVESGALQVKKM 120
QY 121 PKTRPPINVKIIEGLKAVLPCTTMGNPKPSVSNIKGDSPLRENSRIATVLESGLRIHN 180
Db 121 PKTRPPINVKIIEGLKAVLPCTTMGNPKPSVSNIKGDSPLRENSRIATVLESGLRIHN 180
QY 181 OKEDAGGYRCVAKNSLTAAASKVYKLEFEVFARILRAPESHNVTGFSVYLHCATGIPV 240
Db 181 OKEDAGGYRCVAKNSLTAAASKVYKLEFEVFARILRAPESHNVTGFSVYLHCATGIPV 240
QY 241 PTTIWIENGNAVSSGSIQESVKDRVIDSRLOLFTFKPGLYCIATNKHGEKFSATAKAAT 300
Db 241 PTTIWIENGNAVSSGSIQESVKDRVIDSRLOLFTFKPGLYCIATNKHGEKFSATAKAAT 300
QY 301 ISTAEMSKPOKDNKGCAQYRGVCAVNL-----AKDALVEL-NTSYADPEBAQELLVHT 354
Db 301 ISTAEMSKPOKDNKGCAQYRGVCAVNL-----AKDALVEL-NTSYADPEBAQELLVHT 354
QY 355 AMNELKAVSPVCRPAALALCNHIFQECSPGVPTPIPIGREGYCLAVKELCAKEMLYME 414
Db 355 AMNELKAVSPVCRPAALALCNHIFQECSPGVPTPIPIGREGYCLAVKELCAKEMLYME 414
QY 415 EKHARGLYRSEMLLSVPKCSKLPMSHMDPTACARLPHLDYKNENLTFPPMTSSKPSVD 474
Db 415 EKHARGLYRSEMLLSVPKCSKLPMSHMDPTACARLPHLDYKNENLTFPPMTSSKPSVD 474
QY 475 IPNLPSSSSFSYSPIYSMTVIISIMSFRAIVLITITLYCCRRKKQMKKRESAAV 534
Db 475 IPNLPSSSSFSYSPIYSMTVIISIMSFRAIVLITITLYCCRRKKQMKKRESAAV 534
QY 535 TLTLPSELDDLDRHPMPYORBPMLLPKLLSEYPRNNIEYVRDIEGEGAFGVQPARA 594
Db 535 TLTLPSELDDLDRHPMPYORBPMLLPKLLSEYPRNNIEYVRDIEGEGAFGVQPARA 594
QY 595 PGLLPYEPFTMAVKMLKEBASADMDQAFORALMAEFDPNPVTKLLGVCAVSKPCLL 654
Db 595 PGLLPYEPFTMAVKMLKEBASADMDQAFORALMAEFDPNPVTKLLGVCAVSKPCLL 654
QY 655 FETMAVGDLEFLRSMSPHVCSLSHSDLSMRAOVSSPGPPILSCAQLCTARVAAGMA 714
Db 655 FETMAVGDLEFLRSMSPHVCSLSHSDLSMRAOVSSPGPPILSCAQLCTARVAAGMA 714
QY 715 YLSERKEVHARDLATRNCLVGENNVKJADGSLRNISADYKANKENDAIPIRMPPESI 774
Db 715 YLSERKEVHARDLATRNCLVGENNVKJADGSLRNISADYKANKENDAIPIRMPPESI 774
QY 775 FYNRYTTESVYVAVGVVLMIEFSTGLQPYGMAHEEVIYVRDGNILSCPENCVELYNL 834
Db 775 FYNRYTTESVYVAVGVVLMIEFSTGLQPYGMAHEEVIYVRDGNILSCPENCVELYNL 834
QY 835 MRLCWSKLPADRPSPFHSIRHLERMCERAGT 866
Db 835 MRLCWSKLPADRPSPFHSIRHLERMCERAGT 866
QY 837 MRLCWSKLPADRPSPFHSIRHLERMCERAGT 868
Db 837 MRLCWSKLPADRPSPFHSIRHLERMCERAGT 868

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RP SEQUENCE FROM N.A.
RC TISSUE=ELECTRIC ORGAN, AND MUSCLE;
RX MEDLINE=93219391; PubMed=8385349;
RA Jennings C.G.B., Dyer S.M., Burden S.J.;
RT "Muscle-specific trk-related receptor with a kringle domain defines a
RL distinct class of receptor tyrosine kinases.";
DR EMBL: L11311; AAA49285.1; -.
DR HSPG: P11362; IEGK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR000024; F2_domain.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF00051; Kringle; 1.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00018; KRINGLE.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00410; IG_Like; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS50038; Fz; 1.
DR PROSITE: PS00021; KRINGLE_1; FALSE_NEG.
DR PROSITE: PS50070; KRINGLE_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW App-binding; Immunoglobulin domain; Kinase; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 946 AA; 105892 MW; 81A9131DB7479D01 CRC64;

Query Match 63.4%; Score 2897; DB 13; Length 946;
Best local similarity 59.9%; Pred. No. 7.7e-252;
Matches 571; Conservative 113; Mismatches 169; Indels 100; Gaps 11;

QY 5 VNPIVHILTLVAESGTEK--LTPKAVITPPLTVDAIVEEATWCAVESYPOPEISWT 62
Db 6 VDIPLMLTF-LVTGGASDGLTPKAPQITSPLETVDAIVEEATWCAVESYPAETLWT 64
QY 63 RNKILIKLEFDTYSIRENGQLITLISVEDSDGIVCCPTANNNGVGVESGALQVKKPK 122
Db 65 RNNIPIRPFDTRSTKENGQLITLISVEDSDGIVCCPTANNNGVGVESGALQVKKPK 124
QY 123 TTRPPINVKIIEGLKAVLPCTTMGNPKPSVSNIKGDSPLR-ENSRIVLESGLRIHNQ 181
Db 125 IIRPPTVRALILGSKVVLPCSTMGNPAPISWFKDETALKNDDPRTSVLESGLRIHNQ 184
QY 182 KEQDAGYRCVAKNSLTAAASKVYKLEFEVFARILRAPESHNVTGFSVYLHCATGIPV 241
Db 185 LEDAGKTRCLARNSLGEYRSAALEVOVSARIYKAPTSONVSGSEYILQCKATGPIIP 244
QY 242 TTTIWIENGNAVSSGSIQESVKDRVIDSRLOLFTFKPGLYCIATNKHGEKFSATAKAAT 301
Db 245 TIKMLENGRAVPRKGSINRNLKGEVMSRLRYVYRSLFTCLTNKKNESSTAKATATL 304
QY 302 ISTAEMSKPOKDNKGCAQYRGVCAVNLAKDALVELNTSYADPEBAQELLVHTAMNELKV 361
Db 305 DIKEM-RLYKGDGLGCTSTYGEVCOGLLGQOLVFENSSPADDEGTOEMMARSTWELDG 363
QY 362 VSPVCRPAALALCNHIFQECSP-GVPTPIPIGREGYCLAVKELCAKEMLYMEKTHRG 420
Db 364 VSLCKPRAASLLCHFTFOCNPLGLPTKLVCREHCLAVKELCYKEMITMEDNSRIG 423
QY 421 LYSEEMLLSVPKCSKLPMSHMDPTACARLPHLD-----YKNENL----- 460
Db 424 VYSAG---LSLPDQGRLPSTIHPDEACTRVSLDMKKGIVTRMICYNNNGRFYQSVAVTA 480

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QY 461 -----KTEPMTS----- 469
DB 481 SGISCRMBEQAFHFRRLPEPELANSDFCRNPGESERWCYTMORDIMEFCNP 540
QY 470 -----KPSVDIPNLPSSSSSFSFSPYTMVITISMSFAIFLLITLTYCC 518
DB 541 OCINVSSISEMKRTEPTAMPSTSA-----TYSMTVIISISLSLAASILLIITLTC 593
QY 519 RRRKMKNNK--RESAAVTLTLPSELRLDRHPNPMYOMPLLNPKLSTLEYPNNIE 576
DB 594 HHQKGQTRKSYTETETPLATLPSELRLDRHPNPMYOMPLLNPKLSTLEYPNNIE 653
QY 577 YVNDIEGAGRVFOARAPGLLPYEPPTWAVKMLEEASADMQADFOREALMAEFDNP 636
DB 654 YVNDIEGAGRVFOARAPGLLPYEPPTWAVKMLEEASADMQADFOREALMAEFDNP 713
QY 637 NIKKLGVCVAVGKPMCLLFYMAVGDNEFLRSMSPHTCSLSHDSMAQVSSGPP 656
DB 714 NIKKLGVCVAVGKPMCLLFYMAVGDNEFLRSMSPHTCSLSHDSMAQVSSGPP 773
QY 697 LSCAEOLCTARQVAAAGMAYLSERKFVHRDLATRNCLVGENMYVKIADFGLSRNIYSADY 756
DB 774 LSCADQLNTAKQISAGMTYLSERKFVHRDLATRNCLVGEKLVYKIDFGLSRNIYSADY 833
QY 757 KANENDAIPIRMMPESIFNRYTTESDVWAVGVLMETFSYGLQPYGMAHEEVIYVR 816
DB 834 KANENDAIPIRMMPESIFNRYTTESDVWAVGVLMETFSYGMOPYYGMAHEEVIYVR 893
QY 817 DGNILSCPENCPVELYNLMRLCWSKLPADRPSTSIHRIERMCERAGTIVSV 869
DB 894 DGNILSCPENCPVELYNLMRLCWSKLPADRPSTSIHRIERMHQMAALPV 946

RESULT 8
Q9DDA2 PRELIMINARY: PRT: 354 AA.
AC Q9DDA2:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MUSCLE SPECIFIC KINASE, TK DOMAIN (FRAGMENT).
GN MUSK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu A.K., Smith F.D., Zhou H., Chu A.H., Tsai K.W., Peng B.H., Ip N.Y.,
RT "Xenopus MusK: Molecular cloning and prominent expression in neural
RT tissues."
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ222795; CAC19037.1;
DR HSSP: P1362; IFCG
DR InterPro: IPR002919; Euk-kinase.
DR InterPro: IPR002290; Ser_thr-kinase.
DR Pfam: PF00069; kinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; STKC.1.
DR SMART: SM00219; TYRK.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER
SQ SEQUENCE 354 AA; 40410 MW; 87BD2A217D95DDCE CRC64;
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Query Match 35.1%; Score 1602; DB 13; Length 354;
Best Local Similarity 85.3%; Pred. NO. 9.5e-136;
Matches 301; Conservative 21; Mismatches 31; Indels 0; Gaps 0;

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QY 517 CRRRRKMKNNKRRSAVTLTLPSELRLDRHPNPMYOMPLLNPKLSTLEYPNNIE 576
DB 2 CSRKQKTKMKNNKNEAAPITLALPSELRLDRHPNPMYOMPLLNPKLSTLEYPNNIE 61
QY 577 YVNDIEGAGRVFOARAPGLLPYEPPTWAVKMLEEASADMQADFOREALMAEFDNP 636
DB 62 YVNDIEGAGRVFOARAPGLLPYEPPTWAVKMLEEASADMQADFOREALMAEFDNP 121
QY 637 NIKKLGVCVAVGKPMCLLFYMAVGDNEFLRSMSPHTCSLSHDSMAQVSSGPP 656
DB 122 NIKKLGVCVAVGKPMCLLFYMAVGDNEFLRSMSPHTCSLSHDSMAQVSSGPP 181
QY 697 LSCAEOLCTARQVAAAGMAYLSERKFVHRDLATRNCLVGENMYVKIADFGLSRNIYSADY 756
DB 182 LSCADQLNTAKQISAGMTYLSERKFVHRDLATRNCLVGENMYVKIADFGLSRNIYSADY 241
QY 757 KANENDAIPIRMMPESIFNRYTTESDVWAVGVLMETFSYGLQPYGMAHEEVIYVR 816
DB 242 KANENDAIPIRMMPESIFNRYTTESDVWAVGVLMETFSYGMOPYYGMAHEEVIYVR 301
QY 817 DGNILSCPENCPVELYNLMRLCWSKLPADRPSTSIHRIERMCERAGTIVSV 869
DB 302 DGNILSCPENCPVELYNLMRLCWSKLPADRPSTSIHRIERMHQMAALPV 354

RESULT 9
Q9V6K3 PRELIMINARY: PRT: 724 AA.
AC Q9V6K3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BDNF/NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB
DE TYROSINE KINASE) (NEUROSPECIFIC RECEPTOR TYROSINE KINASE) (NRK
DE PROTEIN) (CG4007 PROTEIN).
GN NRK OR KOR2 OR HD-434 OR CG4007.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BERKELEY.
RC MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Gelinkher S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferrier W.M., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtens R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveloff J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Frith K.J., Scott M.J.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 17-724 FROM N.A., AND CHARACTERIZATION.
 RC TISSUE-IMAGINAL DISKS:
 RX MEDLINE-97277331; PubMed-9115253;
 RA Oishi I., Sugiyama S., Liu Z.-J., Yamamura H., Nishida Y., Minami Y.;
 RT "A novel *Drosophila* receptor tyrosine kinase expressed specifically in
 the nervous system. Unique structural features and implication in
 developmental signaling,"
 RL J. Biol. Chem. 272:11916-11923(1997).
 RN [4]
 RP SEQUENCE OF 586-638 FROM N.A.
 RX MEDLINE-98401146; PubMed-9731193;
 RA Oates A.C., Wolberg P., Achen M.G., Wilks A.F.;
 RT "Sampling the Genomic Pool of Protein Tyrosine Kinase Genes using the
 Polymerase Chain Reaction with Genomic DNA,"
 RL Blochem. Biophys. Res. Commun. 249:660-667(1998).
 CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
 CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
 CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
 CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
 CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
 CC GAMMA-1 (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURAL CELL LINEAGE FROM
 CC EMBRYONIC STAGE 11 ONWARDS, RESULTING IN EXPRESSION IN THE BRAIN
 CC AND VENTRAL NERVE CORD AT THE END OF EMBRYOGENESIS.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN EMBRYOS AND
 CC LARVAE, LOW LEVELS IN ADULTS AND POBAE SHOW MAXIMAL EXPRESSION.
 CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN
 CC MANY PROTEINS. NUMBER IN THIS PROTEIN: 2.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 DR EMBL; AE003819; AAF58420.1; ALT_INIT.
 DR EMBL; AF031764; AAD02091.1; -
 DR EMBL; AB001420; BAA20134.1; -
 DR EMBL; AJ002920; CAA05755.1; -
 DR HSSP: P11362; IFG.
 DR FLYBase; FBgn0020391; NrK.
 DR InterPro; IPR000719; Euk_kinase.
 DR InterPro; IPR000024; Fz_domain.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF00051; Kringle; 1.
 DR Pfam; PF00069; kinase; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00219; TKC; 1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS00021; KRINGLE_1; FALSE_NEG.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;
 KW Phosphorylation: Receptor; Glycoprotein; Neurogenesis; Leucine-repeat;
 KW Repeat: Immunoglobulin domain; Developmental protein; Signal.
 FT SIGNAL 1 11
 FT CHAIN 12 724
 FT DOMAIN 12 322
 FT TRANSMEM 323 343
 FT DOMAIN 344 724
 FT DOMAIN 48 83
 FT REPEAT 48 61
 FT REPEAT 62 83
 FT DOMAIN 172 223
 FT DOMAIN 243 279
 FT DOMAIN 441 711
 FT NR_BIND 447 455
 FT BINDING 475 475
 FT ACT_SITE 580 580
 FT MOD_RES 606 606
 FT MOD_RES 610 610
 FT MOD_RES 611 611
 FT SITE 419 419
 FT SITE 721 721
 FT SITE 721 721
 FT CONFLICT 51 51
 FT CONFLICT 192 192
 FT CONFLICT 306 306
 FT CONFLICT 387 387
 FT CONFLICT 391 391
 FT CONFLICT 547 547
 FT CONFLICT 706 724
 SQ SEQUENCE 724 AA; 81836 MW; 0FFB9E1F7E4F6A26 CRC64;
 Query Match 24.7%; Score 1129.5; DB 5; Length 724;
 Best Local Similarity 38.0%; Pred. No. 1.2e-92;
 Matches 263; Conservative 81; Mismatches 174; Indels 175; Gaps 21;
 QY 310 QDNKGYCAQYRGECVNAVLAKDALVPLNTSYADPEEA--OELLVHTAMNEL-KVSPVC 366
 DB 63 ERENGCYAPSGKCKRYLYLGQWY----SLEPDTGKMKNQYTTALMDLISDTGLC 118
 QY 367 RPAEALLCNHIFQPC-SGYVPTPIPICREYCLAVKELFAKELVWEETHGLYSE 425
 DB 119 REAAEKMLCAYAFPCNHEGGRAYAPLCFEDCAATHLDFCYNDVWLIEEKERNMFTKS 178
 QY 426 MHLISVPCSKLPMSHMDPTACARLPHDY-----N 456
 DB 179 RGHFRLPNCSSLP--HYN-ASMRPNCSTYIGLEIKSEVSYDCRNGNGAFYGMTNYS 234
 QY 457 KENT-----KTF-PPWT-----SKRP-----SVDI 475
 DB 235 KSGIPCQWMDTQYPRKHQPLVLFHQLEGENYCRNAGGERPHPCYTVDESVMQHCDI 294
 QY 476 P-----NLBSSSSSSSVSPYSMTVLTISMSFAIFVL-LITTLTYCCRR 521
 DB 295 FMCPRDYVDPAVDLNTPIKMEKF--TPSMFLLAGIGFAVLTALMLTLVYKSKH 350
 QY 522 KQWK-----NKKRE-----SAA 533
 DB 351 KDYSOPAGAAVDECSVSKRGCGGNGNINTSRETLGGNGNTNLAKGCTIRSTATHSNC 410
 QY 534 VTLTLPSELLDLRLHPNMYQRMPLLNPKLISLEYPNNIEYVRDIGEGAFGRVPOAR 593
 DB 411 VALTTVTN--VSDAKGTR-----NARLEKLEYRGDIYVYRSIGGAFGRVPOAR 459
 QY 594 APGLIPEPFTMAVAKMKKEASADMQADFQREBALMAEDNPNTVKILGYCAVKGKPMCL 653
 DB 460 APGLVPDQEDDLVAVKMKKDDASDMQDFEREACILAEFDHPNIVRLIGYCALGRPMCL 519

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OY 654 LFEYMAVGDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPGPPPLSCAEQLCIARQVAAGM 713
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 LFEYMAVGDLNEFLRACSPFAVTHQAPTD---RLQLNE-----LHLLOMANIAGM 568
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 714 AYLSERKFPVARDLNRCLVGENMVKIADFGISRNYSADYKANKANDAPIRMPPES 773
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 569 LYLSERKFPVARDLNRCLNENHMAVKIADFGISHKIYLQDYKCGENDEPIRMPPLES 628
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 774 IFYRRTYTESDVAAVGVLMVEIFSYGLOPYYGMAHEVIYVVRDGNLSCPEMCPVELYN 833
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 629 ILNKSLESVDWAVYICILMEVFSFALQPPFGLTHERVYKTYKEGNVLGCPDNPUSVA 688
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 834 LMRCLWSKLPADRPSPFTST----HRIERMCE 861
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 689 LMRCLWSKLPADRPSPFTST----HRIERMCE 861
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
OY 09BKL8 PRELIMINARY; PRT; 1145 AA.
ID 09BKL8;
AC 09BKL8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ROR.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anasplidae;
OC Aplysiidae; Aplysia.
OX NCBI_TaxId=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA McKay S.E., Hsiolop J., Scott D., Bulloch A.G., Kaczmarek L.K.,
RA Carew T.J., Sossin W.S.;
RA "Aplysia for, a member of the Trk/Musk family of receptor tyrosine
RT kinases, forms clusters on the surface of identified neuroendocrine
RT cells.";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL; AF216782; AAK25726.1; -.
DR HSRP; P11362; 1FGK.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR003599; 1g_.
DR InterPro; IPR003599; 1g_.
DR InterPro; IPR003598; 1g_c2.
DR InterPro; IPR003600; 1g_1like.
DR InterPro; IPR003606; 1g_mhc.
DR InterPro; IPR000001; Kintigle.
DR InterPro; IPR002011; Receptor_tyr_kin_II.
DR InterPro; IPR002290; Ser_thr_Pkinase.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00047; 1g; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG_1like; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKIC; 1.
DR PROSITE; PS50036; Fz; 1.
DR PROSITE; PS50031; KRINGLE_1; UNKNOWN_1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Transferase; Transmembrane.
SQ SEQUENCE 1145 AA; 125622 MW; 5C49FA6E2A9D1ABD CRC64;

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Query Match 21.2%; Score 966.5; DB 5; Length 1145;
Best Local Similarity 30.7%; Pred. No. 1,2e-77;
Matches 265; Conservative 99; Mismatches 278; Indels 221; Gaps 26;

OY 129 NVKTIKELKAVLPCTMTGNPKPSVSWIK-----GDSPLRESRITAVLESGS 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 92 NVTKYGAQVARIICETLTGNPIPIYSWKDYIITNDBSDRMCHKPTAMGR----- 143
OY 175 LRIHNVQKEDAGQRCVAKNLSGTAYSKVYKLEFEVFAIRLARPESHNVPFGSEVTLHCT 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 LKINDVRSPDSAVYTCKAENDFC-----NEETSGSLTVLENEN 180
OY 235 ATGIPVPTTIWINGNAVSSGSIQESYKDRVIDSRQLQFTTKRGTYCTIATNKHGEKFT 294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ---PPP-----SKSGGGSNNDDVDVPTDVT-----VEGGEFKRRDYT 215
OY 295 AKAAATISIAEMSKPOKDNKGCAOYRGEVCNVLAKDALVFLNTSYADPEEAOELLVHT 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 216 SVWPKDDVDVEDDKPR---DGFQITRGSTCAKFGVGMSTIYVTKLQSRAEKYMARA 272
OY 355 ANNELKVVSPVCRPAEALCNHIFQEGSPGV-VPTPIPCREYCLAVELFCAKEMLYM 413
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 VIQASSHMSQRCQOYGIQSLCYHAFPLCDKTDAPRPRIKCRDECLAENDICRTETYM- 331
OY 414 EERTHGLYRSEMHLLS---VPRCSKL--PSMHMDPTACARLPHLDYKKNENLTPPMTS 468
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 332 -AKRH-----NLIGDNLPRCSQLQGPGR-EGDNCFIRI-----GMPGGR 370
OY 469 S-----KPSYDIPNL-----PSSSSSEFSVPTYSMTVYISIMSSFAIVLLTTTY 516
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 371 SGRGRKGGNPMNNNGTRDRPRGSGSKSRPTDKDTGKGQGP-----TDVY 421
OY 517 CCRRRQ-----WKN-----KKRESAATVLT---LPS 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 CYTGRGTNYRGEVSVKSGFMCLGKWDGFPPELGDHNHCRNPNRGREDADWCFNDRKMK 481
OY 542 ELL-----LDRLHPNP-----MYORMPL----- 560
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 ELCAVPRKCDYDEGHRSEADSGSNKMLTILISLTYPLALGILALICCSQSHNTRASR 541
OY 561 -----LNPKLLS--LEYPRNNIEYVRDIEGAGFGRVQARAPGLPYEPPTM 605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 PNKQAQPVEMSLPKKASRAREFPMPIRFLDELGEAGFVKYKGLVYGESSVTT 601
OY 606 VAVKMLKEEASADMOADPQREAAIMAEFNPVIVLIGVCANCKPRCLLFETMAQGLNE 665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 602 VAKTLKENALPKVQNDRRREVDLMSDMRHPNIVCLGVCMKQEPWCMLEFYMAQGDLE 661
OY 666 FLRSMSPHTVCSLSHSDLSMRAQVSSPGPPPLSCAEQLCIARQVAAGMAYLSERKFVARD 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 662 YLLSHSPHSVDYTAABDD-----SGTGGGHLLEYSEMLHVSQVAAGMYLASHNPFVARD 715
OY 726 IATRCVLGENMVKIADFGISRNYSADYKANKANDAPIRMPPESIFVRYRTTESDV 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 716 IAAKNILVAADGLTVKISDFGSLSDYVSSDYVQSKSLPVWMPMPREALYKFTTDSY 775
OY 786 WAYGVLMVEIFSYGLOPYYGMAHEVIYVVRDGNLSCPEMCPVELYNIMRLCWSKLPAD 845
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 776 WAFGVLMVEIFSYGLOPYYGMAHEVIYVVRDGNLSCPEMCPVELYNIMRLCWSKLPAD 845
OY 846 RPSFTSHRIERMCEAEGTVS 868
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 836 RPPFREIHTRLTW--RSELTTS 856
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
OY 09YH44 PRELIMINARY; PRT; 821 AA.
ID 09YH44;
AC 09YH44;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

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DE NEUROTROPHIN RECEPTOR B XTRKB-ALPHA.
GN XTRKB.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97101727; PubMed=8946245;
RA Islam N., Gagnon F., Moss T.;
RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb
RT mRNA are expressed in a pseudo-segmental manner within the early
RT Xenopus central nervous system.";
RL Int. J. Dev. Biol. 40:973-983(1996).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: U39670; AAD0001.1; -.
CC HSSP: P06213; IIRK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00560; LRR; 1.
DR Pfam: PF01463; LRCT; 1.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00409; IG; 1.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00013; LRNT; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
DR ATP-binding: Glycoprotein: Phosphorylation; Receptor; Transferase;
KW Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 821 AA; 92311 MW; 0AF81BEF4FD8FED3 CRC64;

Query Match 17.6%; Score 802; DB 13; Length 821;
Best Local Similarity 27.5%; Pred. No. 4.8e-63;
Matches 239; Conservative 102; Mismatches 241; Indels 286; Gaps 24;

QY 24 LPRAPVITTPLETVDALVEEATMCAVESTPPEISITRKILIKLFDTRYSTIRENGQL 83
b 196 LPIANVSTV---NITVLEGNETTLYCDANGLPDPNVSWDIOISK--KREMAKRPVL 249
QY 84 LTIISVEDSD-GIYCCFANGVG---AVESGALOVKMKPKITRPIINKIIEGLKAV 139
DB 250 LTLNANVSLDKRLITVCAENSVGDHISV---LNVHPPVITF--IDLPITDH-HWC 302
QY 140 LPCTTMNPKPSVSMI-KGD-----SPLRENSRIAVLESGLRIHNVQKEDAGCYR 189
DB 303 IPFVSRGPKPTLQWFMHGNILSETDFWSKIHETSNYTSNHHGLOLDSPTHLNNGHYT 362
QY 190 CVAANSIGTASKYVKLEFEVFAILIRPESHN-VTSGFTLHCTAGICVPTTWLEN 248
DB 363 LRAENITG-----RDRSISALFMKGPDPGNPTTDPGFYDETSDIG-GTSDIGT 414
QY 249 G--NAVSSGSIQSVKVRIDSRQLPITKPGLYTCIAIKKHG--EKFSTAKAAATISI 303
DB 415 GVTSTDSVNSNGNEDSITVYVVGIAALVCT--GLVIMILLKPGHSGKSGSSVLS- 471
QY 304 AEWSKPKQDNKGCAQYRGECVNAVLAADALVFLNTSTADPEAOELLVTHAMNKLKAYS 363
DB 472 -----NDDDSAS 478
QY 364 PYCRPAEALLCNHIFQSCSPGVVPTPIPIGREYCLAVKELFCAKEMVLWMEKTRHGLYR 423

DB 479 PL-----HHI-----SNG----- 486
QY 424 SEHHLSVPCSKLPSMHPPTACARLPHUDYKENIKTFPMTSSKPSVDIPNLSSSS 483
DB 487 -----SNTSSSE 494
QY 484 SSFVSPTYSMFVILISMSFAIFVLLTITLYCCRRRQKMKKRESAAVLTTLPSL 543
DB 495 GG-----PDYILGM----- 504
QY 544 LLDRLHPNPKYQRPPLLNKLLSL-----EYPRNNIEYVDIGEGAFGVQ 591
DB 505 -----TKIPYIENQYFGITNSHLKSDTFVQIHRIHNIIVLKRLEGEGAFGVFL 553
QY 592 ARAAGLLPYEPFVVAVKMLKEEASADMOADFOREALMAEFDNPINVKLLGYCAVAKPM 651
DB 554 AECYNLYPEQDKILVAVKTLK-DASDNARQDFHREALNLNIGHEHIVKRYGCVESDPL 612
QY 652 CLTFEYVAYDNLNEFLRSMSPHTVCSLSHSDLSMRAQVSSGPPPLSCAQLCIAROVAA 711
DB 613 IMVEYMKHGDINKFLRAHGPDAV-----LMAEGNRPAELTOSOMLHTAQOIAA 661
QY 712 GMATLSERKTVHRLATRNCLVGENMYVKTADFGLSRNIYSADYVKANENDAPIRMP 771
DB 662 GMVYLASQHEVHRDLATRNCLVGENLLVKTIGDFQMSKDVSTDTYRVGGHTMLPIRMMP 721
QY 772 ESIFYNRYTDESQVAYGVVLMELFSGYGLQPYGMAHEEYIYVVRDGNILSCPNCPVEL 831
DB 722 ESIMYKRFTTESDVMSLGAVLMELFTYGKQDPWYLSNNVEYECITQGRVLRPRTCKREV 781
QY 832 YNMLRLCWSKLPADRPSTSIHRLERK 859
DB 782 YDLMIGCQWOREPHMRILNIKEIHSLLQNL 809

RESULT 12
IDYH43 PRELIMINARY; PRT; 811 AA.
AC Q9YH43;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE NEUROTROPHIN RECEPTOR B XTRKB-ALPHA.
GN XTRKB.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97101727; PubMed=8946245;
RA Islam N., Gagnon F., Moss T.;
RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb
RT mRNA are expressed in a pseudo-segmental manner within the early
RT Xenopus central nervous system.";
RL Int. J. Dev. Biol. 40:973-983(1996).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: U39671; AAD0002.1; -.
CC HSSP: P06213; IIRK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00560; LRR; 1.
DR Pfam: PF01463; LRCT; 1.
DR Pfam: PF00069; Pkinase; 1.

DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00409; IG: 1.
 DR SMART: SM00082; LRCT: 1.
 DR SMART: SM00013; LRNT: 1.
 DR SMART: SM00219; TYRKC: 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;
 DR Transmembrane; Tyrosine-protein kinase.
 KM SEQUENCE 811 AA; 91249 MW; CE7CDICF132C1CFS CRC64;

Query Match 17.5%; Score 801; DB 13; Length 811;
 Best Local Similarity 28.5%; Pred. No. 5,9e-63;
 Matches 237; Conservative 104; Mismatches 243; Indels 248; Gaps 27;

83 LTTLSVEDSDGIYCTTANNG---VGGAVESGALQYKMKPKITRPINVKIIBGLKA 138
 161 LLETNLNENONHCFNKKKIPLFNMHHPGCL-----PIAVSTVNTIVLEGNET 214
 139 VLPCPTMGPKPSVSKIKDPLRENSRIA---VLESGSLRIHNVOKEDAGO-YRCVAKN 194
 215 TLVCADANGLPDPNVSDISOISKREMAKRPVL---LTLKNVYSLDNKRITIVCAEN 270
 195 SLGTAVSKVVKLEFEV-FARILLAPESHVNTGSEFVTLH---C---TATGIPVPTTWIE 247
 271 SVGEDH---ISVELNVHPPV-----ITFDLPFLDHHCIPPSVKNRPKPTLQWPH 319
 248 NGNAVSS-----GSIOESYKDRVIDSRLOLFTTKGPLYCIATANKH 288
 320 EGMILSETDPIMSKIHETSNVTSEHNGCLD-----LDSPRTL---NNGFYLRANENY 369
 289 GEKFTSTAKAATISTEMSKPKQKNGCYCAQYRG---EVCNAVLAADALVFLNTSTADEE 345
 370 G-----ROERSISALPMKGRDDYETSTNDIGTSTIGTGTSTD----- 410
 346 EAQELLVHTAMNELKVSPYCPRAEALLCNHIFQCSGCVVPTPIPICREYCLAVKELF 405
 411 ---VSNQGNEDSTIVVVVVGIA-ALVCTGL----- 436
 406 CAKEMLMEEKTHRGLYRSEMHLLSVKCSKL---PS--MHWDPTACARLPHLDYKNEN 459
 437 ---VIM-----LTLKFGRRSKFGLKPPSSVSNDDSDASPLHHISNGS-- 477
 460 LKTFPMTSKPSVDLPNLPSSSSSFVSPTYSMTVIISIMSFAIVLTTITLXCCR 519
 478 -----NTPSSSEG-----PDVVIIGM----- 494
 520 RRMQMKKKRESAAVTLTLPSSELLDLRLHPMYQRMPLLNPKLLSL----- 568
 495 -----TKIPPIENPQVFGAIIINSLKSDTFV 519
 569 -EYPRNNIEYVDIGEGAGRGVFOARAPGLPYEPPTMAVAKMLKEASADMQADFOREA 627
 520 QHTRNNIYVLRLEGAGRGVFLACYNLYPEQDKILVAVKTLK-DASNNARKDHFREA 578
 628 ALMAEDNPRIYVLLGVCAVGRMCLLEFMAYGDNELPFRSMSPHTVYGLSHSDLSMRA 667
 579 ELLTNLQHEITVFGVCEGDDPLIVFEYMKHGDNLKFLRAHGPDV-----L 627
 688 QVSSPPPLSCAEOLCIAROVAGAAVLSERKEFVRDLATRNCLGVENNVKLTADGSL 747
 628 MARGNPAELTQSOMLIHQIAAGVYLLASQHFVRDLATRNCLGVENNVKLTADGSL 667
 748 RNTYSADYKANENDAIPTFMPPPESTFNRYTSESDVAAYGVVLMETSYGLQPIYGYMA 807
 688 RDVYSTDYAVFGCHTMLPTFMMPPESTFNRYTSESDVAAYGVVLMETSYGLQPIYGYMA 807
 808 HEVYIYVVRGNLTSCENCPVELYNLMRLCMGSKLPADRSFTSHRIELRM 859
 748 NNEVIECTIGRVLQRPRTCPKEVYDMLGCMQREPHMLRIKEIHSLONL 799

RESULT 13
 ID 075682 PRELIMINARY; PRT; 839 AA.
 AC 075682;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE TRKC PROTEIN.
 GN TRKC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98449483; PubMed=9778053;
 RA Ichaso N., Rodriguez R., Martin-Zanca D., Gonzalez-Sarmiento R.;
 RT "Genomic characterization of the human trkc gene."
 RL Oncogene 17:1871-1875(1998).
 CC -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC EMBL: AJ224521; CA12029.1; -.
 DR EMBL: AJ224522; CA12029.1; JOINED.
 DR EMBL: AJ224523; CA12029.1; JOINED.
 DR EMBL: AJ224524; CA12029.1; JOINED.
 DR EMBL: AJ224525; CA12029.1; JOINED.
 DR EMBL: AJ224526; CA12029.1; JOINED.
 DR EMBL: AJ224527; CA12029.1; JOINED.
 DR EMBL: AJ224528; CA12029.1; JOINED.
 DR EMBL: AJ224529; CA12029.1; JOINED.
 DR EMBL: AJ224530; CA12029.1; JOINED.
 DR EMBL: AJ224531; CA12029.1; JOINED.
 DR EMBL: AJ224532; CA12029.1; JOINED.
 DR EMBL: AJ224533; CA12029.1; JOINED.
 DR EMBL: AJ224534; CA12029.1; JOINED.
 DR EMBL: AJ224535; CA12029.1; JOINED.
 DR HSSP: P06213; 1IRK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003589; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR002011; Receptor_tyrl_kin_II.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; LRR; 1.
 DR Pfam: PF00560; LRR; 2.
 DR Pfam: PF01463; LRCT; 1.
 DR Pfam: PF01462; LRNT; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00082; LRCT; 1.
 DR SMART: SM00013; LRNT; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR ATP-binding; Glycoprotein; Phosphorylation; Receptor; Transferase;
 KM Transmembrane; Tyrosine-protein kinase.
 SO SEQUENCE 839 AA; 94428 MW; 7FE8846830083C08 CRC64;

Query Match 17.3%; Score 792.5; DB 4; Length 839;
 Best Local Similarity 25.9%; Pred. No. 3.6e-62;
 Matches 254; Conservative 125; Mismatches 244; Indels 357; Gaps 38;
 6 NPLVHI-----LTLVAFSGNEKL-----PAAPVITPPLTVDAVVEE 43
 79 NITSIHENKRSILTNAAVMELYTGLQKLTINSGLRSIQAPAFKAPHLRIINLSSNR 138

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QY 44 VATECAVESYPOPEISWTRKILKLEDTYSIRENQULLTILSVED----- 91
DB 139 LTT-----LSW-----QLFOT--LSLRE-----LQLEQNFENCSCDIRM 171
QY 92 -----SDDGIYCCCTANNGVGA-----VSSCALOVKMKPKITRPINVKI 132
DB 172 QLMDOEGEAKLNSQMLYICIND-----GSQPLFRNNISQCDL-----PEISVSHVNLTV 221
QY 133 IEGLKAVLPCTTGMNPKSVSWI-----KGDSPLENSRLAVESGLRIHNVQKEDAG-Q 187
DB 222 REGDNAVITTCNGSGSPLEDDVIMIVYGLSINTHOTNLMTWVHAINLTLVNTSEDCFT 281
QY 188 YRCVAKNSLG-----TAY--SKVYKLEFEVFAIRILRADE--SHNVFGSEVTLTCT 234
DB 282 LTCIAENVGSMNSVALTYVPPRVSL-----EPRLREHCHIEF-----V 324
QY 235 ATGIVPPTITMENGNVSSGI--QESVKDRVIDSLQLTLTKP-----GLYCIATNK 287
DB 335 VRGNPPTLHMLHNGOPLRESKILHVEYQGEISEGCLLP--NKPTHYNNGNNTLIAKNP 383
Y 288 HGEKSTAKAATITIAEMSKPQKDKNGCYCAQYRGECNVANLAKALVFLNTSYADPEEA 347
DB 384 LG-----TAQOTIN-----GH-----FLKEPF--PEST 404
QY 348 QELLVHTAMNELKVVSPYCRPAEALLCNHIFOECSPEGVPTPIPICREYCLAVELECA 407
DB 405 DNF1-----LEDEVSP----- 415
QY 408 KEMLVMEKTRGLRYSRMLHLSVPKCKSLPSMHMDPTACARLPHLDYKNENKLTTPPMT 467
DB 416 -----TPBIT 420
QY 468 -SSRPVDYVNLPSSSSSSFVSPTYSMTVTIISMSFAIFVLLITTLCCRRRCKOKN 526
DB 421 VTHRPEED-----TFGVSIYVGLAARFACVLLVLFVWINKYGRSKNGM 464
QY 527 K-----KRESAAVTL-----TTLPELLELDRLHPNPM--YORMPLNPKILLSLEY 570
DB 465 KGPYAVISGEDSASPLHINHNGITTPSSL--DAGPDTYVIGMTRIPVIEINPQYFRQHG 521
QY 571 -----PRNNIEYVDIGEGAFRGYFQARARPELLEPFTYVAVYVAMKLEASAD 618
DB 522 NCHRPDTYVOHKKRDLVLRLEDEGAGKVFLECYNLSTPKDKMLVAVVXALDPTLA- 580
QY 619 MOADFQREALAMAEFDPNINYLKLGCAVGRKMLLEFYAAYGDLNEFLRSMSPHTVCSL 678
DB 581 ARKDFQREALLTNLOHNIHIVKFGVCGDGPLIMVPEYMKHODLNFRLRAGHD----- 635
Y 679 SHSLSMRAQVSSPQPP-----PLSCAEQOLCIAROVAAGMAYLSEKRFVHRDLATRNCLV 733
DB 636 -----AMILVGOGPROAKGELGSLQMLHIASQIASGMVYLASQHFVHBDLATRNCLV 687
QY 734 GENNVYKIDFGLSRNYSADYK--ANEND-----AIPRMPPESEIFNRY 779
DB 688 GANLVVKGIDFGMSRDVYSTDYKFLNPSGWDCEICWEGVGHYMLPIRMPPESEIMRK 747
QY 780 TTESDVAVYGVVLEIFSYGLQPYGMAHEVIVYVRDGNILSCPEKCPVELYMLMLCWM 839
DB 748 TTESDVAVSFGVILWEITFYGQPFQLSNTEVICITQGRVLERPRVCKREVIYVMLCGW 807
QY 840 SKLPADRPSTSIHRIERM 859
DB 808 QREPOQRLNIKEIKLIAL 827

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RESULT 14
Q24488 PRELIMINARY; PRT; 685 AA.
AC Q24488;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

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DE TYROSINE-PROTEIN KINASE TRANSMEMBRANE RECEPTOR ROR PRECURSOR
DE (EC 2.7.1.112).
GN ROR OR CG4926.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RC STRAIN=CANTON-S; TISSUE=LARVAL BRAIN;
RX MEDLINE=9348222; PubMed=8394009;
RA Wilson C., Guberhan D.C.I., Steller H.;
RT "Drosophila: a potential neurotrophic receptor gene, encodes a Drosophila
RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine
RT kinases.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis J.R., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brooksstein P., Brotler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garcia N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mohrson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Stryckas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 545-597 FROM N.A.
RX MEDLINE=98401146; PubMed=9731193;
RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
RT "Sampling the genomic pool of protein tyrosine kinase genes using the
RT polymerase chain reaction with genomic DNA.";
RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR THAT FUNCTIONS DURING
CC EARLY STAGES OF NEURONAL DEVELOPMENT.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONS OF THE DEVELOPING NERVOUS
CC SYSTEM.

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DR PROSITE, PS50038; FZ: 1.
 DR PROSITE, PS50070; KRINGLE_2; 1.
 DR PROSITE, PS50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE, PS50111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS50109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Immunoglobulin domain; Kinase; transferase.
 SQ SEQUENCE 928 AA; 103864 MW; F13B8C9BCAB30D20 CRC64;

Query Match 16.9%; Score 773.5; DB: 5; Length 928;
 Best Local Similarity 24.7%; Pred. No. 2.2e-60; Indels 275; Gaps 32;
 Matches 237; Conservative 139; Mismatches 309;

QY 87 LSVEDSDGIGYCCFANGGAGVAVGALGVKMP--KTRPPINVKIIEGLKAVLPCTT 144
 DB 10 LVLEPADD-----EGLHGNASMEGTSGORPYIRLTQLNRNATKSSGDEVFRKCEA 61
 QY 145 MGNRPVSVWIKGDSPLRENSRIAVLE---SGSLRIHNVKEDAGQRCVAKNSLGTAYS 201
 DB 62 LGTEPLKFIWKNNGPVEKTRKVRKIRDKENSSRLVITQDLDSGYQCIYSNPAASVNT 121
 QY 202 KVKLEFEVFRILRAPE-----SH---NVTFGSEVTLHCTATGIPPTIWIEN 248
 DB 122 TSV-----LRVNNVPAAVLSOKGSHSTKHIAFDEY-----ED 156
 QY 249 GNAVSSGSI---QESVKDRVIDSLQLFTPKGLYTCIATNKHGEKSTAKAATISTAE 305
 DB 157 YEMDRGRLLPDEEDADLRVPDS-----AAGSNVAPAVASE 192
 QY 306 -WSRPQKNKGYCAQYRGECNAVLAKDALVELNTSYADPEE-----AOELLVHTANNE 358
 DB 193 RMLDGIRKRVGDCVQYRGACROYLSNKFVAMTNSREMYDIDRLNLAAMLF-----NG 248
 QY 359 LKVVSPVCPAAEALLCNHIFQECSPGVVPPPIPCREYCLAVELFCAKEWLVME--- 415
 DB 249 APTISQKCRQLSQAVACHHMYKVCESDSNNQIVSICKHDCVITQNDCEPSELALAAQHLE 308
 QY 416 --KTRGLYRSMHLLSVKCKSLPS-----MHW----- 442
 DB 309 VGDTPKALF-----PLCSRLLSTSNICIPYMTALOSSPVAEYNRGHLTHWCYVNSG 359
 QY 443 -----DPTACARLPHLDYNKE--NLKTP-----PMTSKP 471
 DB 360 TQYEGVNAQTSSGKQCA--PWIDSTSRDNVHRFELMNSKNYCRNPGKSRPWCYSKP 417
 QY 472 S-----VDIPNLPS-----SSSSFSVPTYSMTVLIISMS--FA 505
 DB 418 MGOEYCDVPQCPDMDYPHLNDKVEGSKGCVSESVTALMDSLDPTMOVALVGGSVFS 477
 QY 506 IFVILITITLCCRRRKQKMKKRESAAVLTLPSEL-----LLDR 547
 DB 478 LLLLLFCACCCRAKK--KSKQTRHQNAHSSAPSVINSANASAYYRKLTNGSTPIMGR 535
 QY 548 LHPN-----PMYQRMPLLNPKLLSLEYPRNNIEY-----VRD- 580
 DB 536 VPHVEMTSLIPSAQHLGPPYPMDQLQOARFPPOEPLDINSYKVFETTPQSLSVREK 595
 QY 581 IGGAGRGVYFOA--RAPGLLPYEPFTWAVAKLKEASADMQADFOREALMAEFDPNIV 639
 DB 596 IGGGQGVVHSGIYTSGLFAPRPM--VAVKCKHDATNAERAOLEDQIRAVATFDHPNVI 654
 QY 640 KILGCAVGRKMCLEFYMAVYGLNEFLRSMSP---HTVCSLSHSDLSMRAQVSSPPPP 696
 DB 655 KLIGVCYMDNSLAVFEYVHGDHLELKVVPADHDGITEAN----- 700
 QY 697 LSCAEQCLIRQVAAAGAAVYSEKRFVHDLATRNCLIGENNVYKIADEGLSRNYSADYY 756
 DB 701 ---AEFLYIAQIALGLEYLASMSFVRDLATRNCLVGDTRTIKINADFGLMRTSYGSDYY 757
 QY 757 KANENDAIPIRMPPESIFNRYTTESDVAVYGVVLEIFSYGLQPYGMAHEVYIYVR 816
 DB 758 KMLHRSMYPRWMSKEAIEDGRFSEASDVMSFVTLMEIWSFGROPYEGASNOQVIELVA 817

QY 817 DGNILSCPEPCPELYNLNMLRCLSKLPAQRPSFTSI-----HRIERMOCERA 863
 DB 818 NRHLLECPHNCPTNIYISLWECWHENIERRPTSEIRSRLOWSLASPAHSILQQHNNRA 877

Search completed: August 16, 2002, 13:38:33
 Job time: 153 sec

Result No.	Score	Query Match	Length	DB	ID	Description
1	4569	100.0	869	22	AA977856	Protein of muscle Amino acid sequen Humam muscle-specif Rat muscle-receptor Rat Dmk receptor. Mouse muscle-local Mouse muscle-local Nsk2 receptor. Mouse Nsk2 (altern
2	4569	100.0	869	22	AAB66421	
3	4558	99.8	869	18	AAW2611	
4	4558	99.8	869	18	AAW26506	
5	4292.5	93.9	868	18	AAW2610	
6	4292.5	93.9	868	18	AAW26507	
7	4269.5	93.4	868	17	AA92717	
8	4220.5	92.4	860	17	AA92716	
9	4136	90.5	871	17	AAAR84087	
10	4136	90.5	871	19	AAW62568	
11	4128	90.3	881	19	AAW62572	

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		
457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500			
1014	1015	1016	1017	1018	1019	1020	1021	1022	1023	1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1051	1052	1053	1054	1055	1056	1057	1058	1059	1060
1061	1062	1063	1064	1065	1066	1067	1068	1069	1070	1071	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090	1091	1092	1093	1094	1095	1096	1097	1098	1099	1100	1101	1102	1103	1104	1105	1106	1107
1108	1109	1110	1111	1112	1113	1114	1115	1116	1117	1118	1119	1120	1121	1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154
1155	1156	1157	1158	1159	1160	1161	1162	1163	1164	1165	1166	1167	1168	1169	1170	1171	1172	1173	1174	1175	1176	1177	1178	1179	1180	1181	1182	1183	1184	1185	1186	1187	1188	1189	1190	1191	1192	1193	1194	1195	1196	1197	1198	1199	1200	
1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227	1228	1229	1230	1231	1232	1233	1234	1235	1236	1237	1238	1239	1240	1241	1242	1243	1244	1245	1246	1247
1248	1249	1250	1251	1252	1253	1254	1255	1256	1257	1258	1259	1260	1261	1262	1263	1264	1265	1266	1267	1268	1269	1270	1271	1272	1273	1274	1275	1276	1277	1278	1279	1280	1281	1282	1283	1284	1285	1286	1287	1288	1289	1290	1291	1292	1293	1294
1295	1296	1297	1298	1299	1300	1301	1302	1303	1304	1305	1306	1307	1308	1309	1310	1311	1312	1313	1314	1315	1316	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	
1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387
1388	138																																													

	RESULT	1
XX	AAAG77856	
XX	ID	AAAG77856 standard; Protein: 869 AA.
XX	AC	
XX	AAAG77856;	
XX	DT	11-JAN-2002 (first entry)
XX	DE	Protein of muscle specific tyrosine kinase receptor (hmusk-R).
XX	KW	Mutated muscle specific tyrosine kinase receptor; selectable marker:
XX	RW	hmusk-R; human; mmusk-R; antibody; immunoselection.
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FH	Peptide	1..19
FT	/note=	"Signal peptide of hmusk-R"
FT	Protein	20..869
FT	/note=	"Mature protein of hmusk-R"
FT	Domain	20..493
FT	/note=	"Extracellular domain"
FT	Domain	494..515
FT	/note=	"Transmembrane domain"
FT	Domain	516..869
FT	/note=	"Cytoplasmic domain"
FT	Misc-difference	538..869
FT	/note=	"Residues 538-869 are deleted in mutant mmusk-RI"
FT	Misc-difference	577..869
FT	/note=	"Residues 577-869 are deleted in mutant mmusk-RII"
FT	Domain	672..693
FT	/note=	"Kinase catalytic site"
XX		
XX		
NN	WO200172834-A1.	

CC method uses a mutated PKR nucleic acid which comprises a modification
 CC to the intracellular and extracellular domains, or comprises a
 CC modification to the intracellular domain and excludes any nerve growth
 CC factor receptor(s) (NGFR). The method uses mutated PKR as a cell
 CC surface marker, and is useful for identifying genetically modified cells,
 CC especially immunoselection of transduced mammalian cells, and for
 CC identifying mammalian cells expressing a protein of interest. The
 CC genetically modified cells may be used in an autologous or
 CC allogeneic setting e.g. gene therapy for bone marrow transplants, graft
 CC facilitation or immune reconstitution.

XX Sequence 869 AA:

Query Match 100.0%; Score 4569; DB 22; Length 869;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRELVIPLVHITLVAESGTEKLPKAPVITTPLETVDAIVEEATFMCVAVESYPOPEIS 60
 DB 1 mrelvnpjvhlitlvaesgtekpkapvittpletvdaiveeatfmcavesyppeis 60
 OY 61 WFNKLIKLFDRYSIRENGQLLTLSVEDSDGTYCCANNVGAVESGALQVKKM 120
 DB 61 wfnklliklfdrysirengqltltsvedsdgtyccannvgavescgalqvkmk 120
 OY 121 PKITRPINWKITEGLKAVLPCTTMGNPKPSVSMIGDSPLPRENSRIAVLESGLRIHNV 180
 DB 121 pkitrpinwkiteglkavlpcttmgnpkpsvsmikgdsplrensrilavessglihmv 180
 OY 181 OKEDAGQYRCVANKSLGTAVSKVYKLEFEVFAIRILRAPESHNTFGSFVTLHCTATGIPV 240
 DB 181 qkedagqyrcvankslgtavskvyklefevfarilrapeshntfgsfvltlhcatacipv 240
 OY 241 PTTTWENGNNAVSSGSIQSVSDRVDSRLQLEFTRKGLYTCTATNKHGKESTAKAAAT 300
 DB 241 ptttwengnavssgsiqsvsdrvdsrlqlftrkgltyctatnkhgkfstakaaat 300
 OY 301 ISTAENSKFOKDKGCAQYRGEVCNAVLAKDALVFLNLSYADPEEAQELLVHTANNELK 360
 DB 301 istaenskfokdkgcaqyrgevcnavlakdvlfnlscyadpeeaqellvhtannelmk 360
 OY 361 VVSPVCRPAEALLCNHIFQECSPGVVPPPIPIGREYCLAWEKELVMEKTHRG 420
 DB 361 vvspvcrpaeeallcnhifqecspgvvppipicreyclavkelfakewlmeekthrg 420
 OY 421 LVRSSEHLLSVKCSLRPMHMDPTACARLPHLDYKKNKTPRPMTSSKPSVDINDLPS 480
 DB 421 lvrssehlhllsvkcslrpmhmdptacarlphldynkenlktprmtsskpsvdiplnps 480
 OY 481 SSSSSFSVSPYSMTVIISIMSSFAIFVLTITTLVCCRKRQWKKKRSAAVTLTTLTP 540
 DB 481 sssssfsvspysmtviisimssfaifvltittlvccrrkrqwkknkrsaaavtlttltp 540
 OY 541 SELLDRLRPNRYQMPPLLNPKLISLEYPRNNITEYRDIGGAGFGRVQARAPGLLEP 600
 DB 541 sellldrlrpnryqmppllnpkllisleypnniteyrdigagfgrvqarapgllep 600
 OY 601 EFFTVAVMKLEEAQADQADQADQADQADQADQADQADQADQADQADQADQADQADQAD 660
 DB 601 efftvaavmkleeaadqadqadqadqadqadqadqadqadqadqadqadqadqadqad 660
 OY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSPGPPLSCAEQICIAQVAAAGAAVSEKK 720
 DB 661 gdlneflrsmshphtvcsllshsdlsmravspgpplscaeqiclarvaaagaaavsekk 720
 OY 721 FVHRDLATRNCLVGENMVKIADFGLSRNIYSADYYKANENDAPIIRKMPPEISFYNNRYT 780
 DB 721 fvhrdlatrnclvgenmvkiadfglsrniysadykanendapiirmppeisfyynyrt 780
 OY 781 TSSDVAAYCVLWEISYGLQPYGMAHEEVITYYVDGNIILSCPEKCPVELYNLMLCS 840
 DB 781 tssdvaaycvlweisylqpygmaheevityyvdgnilscpencpvelynlmfllcs 840

OY 841 KLPADRPSTSIHRIILERMCEAGETVSV 869
 DB 841 klpadrpstsihriilermceagetrsv 869

RESULT 3
 AAW26611
 ID AAW26611 standard; Protein; 869 AA.
 AC AAW26611;
 DT 27-JAN-1998 (first entry)
 XX Human muscle-specific kinase (Musk).
 DE Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; human.
 KW ligand; agrin; diagnosis; therapy.
 OS Homo sapiens.
 OS MO9721811-A2.
 PN 19-JUN-1997.
 PD 13-DEC-1996; 96WO-US20696.
 PF 10-MAY-1996; 96US-0644271.
 PR 15-DEC-1995; 95US-0008657.
 XX (REGC-) REGENERON PHARM INC.
 PA Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;
 PI WPI, 1997-332783/30.
 DR N-PSDB; AAT90473.
 XX

PT Nucleotide sequences encoding human agrin and muscle specific kinase
 PT and related receptor - used in diagnosis and treatment of disorder
 PT with muscle atrophy
 XX

PS Example 4; Fig 4; 120pp; English.
 XX

XX This polypeptide comprise a novel human receptor tyrosine kinase
 CC designated muscle specific kinase (Musk) that is expressed in
 CC normal and denervated muscle. Musk is alternatively referred to
 CC Dmk for denervated muscle kinase. The amino acid sequence was
 CC deduced from an isolated cDNA clone (see AAT90471). Rat Musk (see
 CC AAW26610) has also been identified. Use of Musk to generate anti-
 CC Musk antibodies and in the diagnosis of neurological or other
 CC disorders is disclosed. Assay systems that may be used to detect
 CC and/or measure ligands that bind the musk gene product are provided.
 CC A claimed method of promoting the growth, differentiation or
 CC survival of Musk receptor-expressing cells involves administration
 CC to the cell of agrin (see AAW26609). Such cells include muscle,
 CC heart, spleen, ovary and retina cells, or cells genetically
 CC engineered to express the Musk receptor.
 XX

XX Sequence 869 AA:

Query Match 99.8%; Score 4558; DB 18; Length 869;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MRELVIPLVHITLVAESGTEKLPKAPVITTPLETVDAIVEEATFMCVAVESYPOPEIS 60
 DB 1 mrelvnpjvhlitlvaesgtekpkapvittpletvdaiveeatfmcavesyppeis 60
 OY 61 WFNKLIKLFDRYSIRENGQLLTLSVEDSDGTYCCANNVGAVESGALQVKKM 120
 DB 61 wfnklliklfdrysirengqltltsvedsdgtyccannvgavescgalqvkmk 120

QY	121	PKTRPPRTNVTIEGKAAVLPCCTMTGMPKPSVSMIKGSDPLREMSRTAVLESGSILRHNV	180
QY	121	PKTRPPRTNVTIEGKAAVLPCCTMTGMPKPSVSMIKGSDPLREMSRTAVLESGSILRHNV	180
Db	121	pkltprlpnvkliegkavlpctctmgnpksvsvikqsdplrenstrlavlesgsltlhmv	180
QY	181	QKEDAGQRCYCAKNSLGTAAYSKVVKLEEFEEFARLRAPESHNVTFGSEFVLHCTATGIPV	240
QY	181	QKEDAGQRCYCAKNSLGTAAYSKVVKLEEFEEFARLRAPESHNVTFGSEFVLHCTATGIPV	240
Db	181	qkedagqrcvaksnlsgtayskvvkleeverfariltrapeshnvtfgsvflhctatgipv	240
QY	241	PTTWIENGNNVSSGSIQDESXKDVIDSRLQLEFTTKGGLYTCAITAKKHGKSTAKAAAT	300
QY	241	PTTWIENGNNVSSGSIQDESXKDVIDSRLQLEFTTKGGLYTCAITAKKHGKSTAKAAAT	300
Db	241	pttlwienngnvnssgsiqeskvkdvldisrlqlftkpglytclatnkhgkislakaaat	300
QY	301	ISIAEWSKPOKDNKGCYAOXRGVEGCNANVLAKDAVFNNTSYPADPEEKOEELVTANNEKL	360
QY	301	ISIAEWSKPOKDNKGCYAOXRGVEGCNANVLAKDAVFNNTSYPADPEEKOEELVTANNEKL	360
Db	301	islaewskpqgkdnkgcycaqyrgvccnaavlakdavlfnstypadpeeqellvhtlanekl	360
QY	361	VSPVPCRPAPALICNHIPOECSPGVVPTPIPICREYCLAIVKELFCAKEMLVNEEKTHRG	420
QY	361	VSPVPCRPAPALICNHIPOECSPGVVPTPIPICREYCLAIVKELFCAKEMLVNEEKTHRG	420
Db	361	vspvpcrpapaaellcnhlfqecspgvvptpripicreyclavkelfcaketwneekthrg	420
QY	421	LYRSMHLLSVPKCSKLPSPMIMDPTACARLPHLDYKNEKTKPPPMSSKSPVDIPLPS	480
QY	421	LYRSMHLLSVPKCSKLPSPMIMDPTACARLPHLDYKNEKTKPPPMSSKSPVDIPLPS	480
Db	421	lyrsemhlsvpckslpsmhwpbtaearlphldynkenktkfpmtsskspvdiplps	480
QY	481	SSSSFSFVSPYSMPTVIIISMSFAIFVLLTTTLTYCCRRRKQWKNKKRESAAVTLTTLIP	540
QY	481	SSSSFSFVSPYSMPTVIIISMSFAIFVLLTTTLTYCCRRRKQWKNKKRESAAVTLTTLIP	540
Db	481	ssssfsfvsytmctvllismsfaifvlltltlyccrrrkqwkknkresaaavltilp	540
QY	541	SELLIDRLHPMPMORPMLINPRLTLELYPRNNIEYVRDIGGAGFGRVQARAPGILPY	600
QY	541	SELLIDRLHPMPMORPMLINPRLTLELYPRNNIEYVRDIGGAGFGRVQARAPGILPY	600
Db	541	sellidrlhpmpmqrmpllnpklisleypnmileyvridgeaigrvtdarapgilpy	600
QY	601	EPPTWVAVKMKLEBASADMDQDFOREALMAEFDNPNTIVALLGVCAVGKEMCLLFEXMAY	660
QY	601	EPPTWVAVKMKLEBASADMDQDFOREALMAEFDNPNTIVALLGVCAVGKEMCLLFEXMAY	660
Db	601	epflmwavakmlkeesaadmqdldfreaalmaefdnplvkllygcavqgkpmcllfeymay	660
QY	661	GDLINEFLRSMKPHRYVCSLSHSDLSMRQVSSPGPPRLSCAFLCIANQVAAAGMYLSEK	720
QY	661	GDLINEFLRSMKPHRYVCSLSHSDLSMRQVSSPGPPRLSCAFLCIANQVAAAGMYLSEK	720
Db	661	gdlineflrsmkphrvcslishsdlsmrqvsppgpprlscacqclclaqvaaagmylsrk	720
QY	721	FVHRDLATRNCLVGENNVVKTADFGLSRNIYSADYVYKANENDAIPIKMPMPESIIFYNRYT	780
QY	721	FVHRDLATRNCLVGENNVVKTADFGLSRNIYSADYVYKANENDAIPIKMPMPESIIFYNRYT	780
Db	721	fvhrdlatrnclvgenmvvktadfglsrnllysadykanendaipikmmpesiifynryt	780
QY	781	TESDWMATGVVLMELFSTYGLDPTRYGMAHEEYIYVRBGNTLSCPBNCPVELYNLMRLCMS	840
QY	781	TESDWMATGVVLMELFSTYGLDPTRYGMAHEEYIYVRBGNTLSCPBNCPVELYNLMRLCMS	840
Db	781	tesdwmagvvlwelfstysgltpbyymgheeyivrvdgntlscpbnpcvelynlmrlcms	840
QY	841	KLPADRPSTSIHRLIERMERCARGTQSVV	869
QY	841	KLPADRPSTSIHRLIERMERCARGTQSVV	869
Db	841	klpadrpstsihrliermercargtqsvv	869
RESULT	4		
AA	AAW26506		
ID	AAW26506	standard; Protein: 869 AA.	
XX	AAW26506:		
AC	AAW26506:		
XX	06-JAN-1998	(first entry)	
DT	06-JAN-1998	(first entry)	
XX	Human Dmk receptor.		
DE	Human Dmk receptor.		
XX	Dmk receptor; tyrosine kinase receptor; signal transduction; assay;		
KW	Dmk receptor; tyrosine kinase receptor; signal transduction; assay;		
KW	therapy; diagnosis; Alzheimer's disease; Parkinson's disease;		
KW	amyotrophic lateral sclerosis; Lou Gehrig's disease;		
KW	idiopathic torsion dystonia; muscle atrophy.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	US5656473-A.		
PN	US5656473-A.		
XX	12-AUG-1997		
PD	12-AUG-1997		

XX		21-JUL-1993;	93US-0095658.	
PF				
XX		19-JAN-1995;	95US-0374834.	
PR		21-JUL-1993;	93US-0095658.	
XX				
PA		(REGE-) REGENERON PHARM INC.		
XX				
PJ		Rojas EA, Valenzuela DM;		
DR		WPI; 1997-414593/38.		
N-PSDB; AAT87073.				
PT		New isolated human denervated muscle kinase receptor - used to		
PT		develop products for the diagnosis and treatment of neurological,		
PT		muscle or neuromuscular disorders		
XX				
PS		Claim 4; Column 31-36; 31pp; English.		
XX				
CC		This polypeptide comprises the human Dmk receptor (AAW26506), a novel		
CC		tyrosine kinase receptor that is expressed in high levels in		
CC		denervated muscle. Its amino acid sequence was deduced from an		
CC		isolated nucleic acid molecule (see AAW7073). The Dmk receptor can		
CC		be used to screen for agents that interact with Dmk. Agents that		
CC		bind to the receptor may mediate survival and differentiation in		
CC		cells naturally expressing the receptor, but may also confer survival		
CC		and proliferation when used to treat cells engineered to express the		
CC		receptor. Dmk receptor polypeptides and polynucleotides can also be		
CC		used for detecting aberrancies in the function or expression of the		
CC		receptor which may be used in the diagnosis of muscular or other		
CC		disorders. Manipulation of the receptor or agonists which bind this		
CC		receptor may be used to treat neurological diseases, diseases of		
CC		muscle or neuromuscular unit disorders, including Alzheimer's		
CC		disease, Parkinson's disease, amyotrophic lateral sclerosis (Lou		
CC		Gehrig's disease), idiopathic torsion dystonia and muscle atrophy.		
CC		The extracellular domain (ECD) of the receptor can be used to block		
CC		the binding of receptor to target cells. A receptorbody comprising		
CC		the ECD fused to a human Ig gamma-1 constant region is claimed.		
XX				
SQ		Sequence 869 AA:		
		Query Match 99.8%; Score 4558; DB 18; Length 869;		
		Best Local Similarity 99.8%; Pred. No. 0;		
		Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps		
				0;
OY		1 MELVNIPLVLHLLTVAESGTEKLPKAPVITTPLETVDALVEEVAFTMCAVSSTYQPETS 60		
DB		1 melvniplvlhlitlvafesgteklpkapiltptlvdalveevatfmcavesypqels 60		
OY		61 WTRNRIILRLPRTFSIRNGQLTLTSLVEDDDGYCTANNNGGAVESGALQVKKK 120		
DB		61 wrnriilrlkflrtfsirngqltlslsveddgdgyctannnggavessgalqvkmk 120		
OY		121 PKRTPRPINVKLIIEGLKAVLPCPTMGNPKPSVSWIKGDSPLENSRIALESGLRHNV 180		
DB		121 pkrtprpinvkliiegkavlpcptmgnpkpsvswikgdsplensrialessglrlnhv 180		
OY		181 QKEDAGQRYCVAKNSIGTAYSKVVVLEFEVFARIIIRAPESHVWTGSFRTLTCGTATGPV 240		
DB		181 qkedagqrycvaknslgtayskvvvlefevfariirapeshvwtgstfrtltcgtatgpv 240		
OY		241 PTTTWENGNNAVSSSIOESVDRYIDSRLOLFITRKPGLYTICATNKHGKEFKSTAANAAT 300		
DB		241 ptttwengnavsssigesvdrvdyidstldqflfkpglytclatnkhgkefstakaat 300		
OY		301 ISIAEMSKPOKDKNKYCAOYRGECNAVLAIAKDALVFLNTSYADPEBAQFLVHTAMNEIK 360		
DB		301 isiaemskpqkdnkycagyrgecnavaiaakalvflntsyadpeeaqellvhtamneik 360		
OY		361 VWSPVCRPAAEALLNNHFQECSPGVVPPIPIIGEVYCAVALCARKMLMEETTHG 420		
DB		361 vwspscrrpaaeallnnhfqecspgvvpvipipigevyclavellcarkwlmeeekthg 420		

OY 421 LKSEMHLLSVPKSKLPSHMDPTACARLPHLDYKNENLKTPEPMTSKPSVDIPNLPS 480
Db 421 LKSEMHLLSVPECKSLPSHMDPTACARLPHLDYKNENLKTPEPMTSKPSVDIPNLPS 480
OY 481 SSSSSFSVSPYSMTVYIISMSFAIFVLLTTITLTCRRRKQWKKKRESAAVLTTLTP 540
Db 481 SSSSSFSVSPYSMTVYIISMSFAIFVLLTTITLTCRRRKQWKKKRESAAVLTTLTP 540
OY 541 SELLDRLHPNPMYQRMPLLNPKLLSLLEYPRNIEYVRDIEGAGRGVQARAPGLLPY 600
Db 541 SELLDRLHPNPMYQRMPLLNPKLLSLLEYPRNIEYVRDIEGAGRGVQARAPGLLPY 600
OY 601 EPTTMAVAVKMLKEASADQADFOREALMAEFDNPNIYKLLGVCAVGKPMCLLFEXMAY 660
Db 601 EPTTMAVAVKMLKEASADQADFOREALMAEFDNPNIYKLLGVCAVGKPMCLLFEXMAY 660
OY 661 GDNELFRMSPHYVCSLSHSDLSMRQVSSPPPLSCAEOCLIAQVAAAGMAYLSERK 720
Db 661 GDNELFRMSPHYVCSLSHSDLSMRQVSSPPPLSCAEOCLIAQVAAAGMAYLSERK 720
OY 721 FVHRDLATRNCLYGENNVVKAIDFGLSRNITYSADYYKANENDAIPIKMPPESTFYRYT 780
Db 721 FVHRDLATRNCLYGENNVVKAIDFGLSRNITYSADYYKANENDAIPIKMPPESTFYRYT 780
OY 781 TESDWAYGVVLEIFSYGLQPYGMAHEVITYVRDGNILSCPEMCPVELYMLRLCWS 840
Db 781 TESDWAYGVVLEIFSYGLQPYGMAHEVITYVRDGNILSCPEMCPVELYMLRLCWS 840
OY 841 KLPADRPFSIHRILERMCEERAGETYSV 869
Db 841 KLPADRPFSIHRILERMCEERAGETYSV 869

RESULT 5
AAW26610
ID AAW26610 standard; Protein: 868 AA.
AC AAW26610;
XX 27-JAN-1998 (first entry)
XX Rat muscle-specific kinase (MusK).
XX Receptor tyrosine kinase; muscle specific kinase; MusK; Dmk; rat;
XX ligand; agrin; diagnosis; therapy.
XX Rattus sp.
XX Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Domain 21..492
FT /label= Extracellular_domain
FT Domain 493..521
FT /label= Transmembrane_domain
FT Domain 522..868
FT /label= Intracellular_domain
XX WO9721811-A2.
XX 19-JUN-1997.
XX 13-DEC-1996; 96WO-US20696.
XX 10-MAY-1996; 96US-0644271.
XX 15-DEC-1995; 95US-0008657.
XX (RECE-) REGENERON PHARM INC.
XX Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;
XX WPI; 1997-332783/30.
XX

DR N-PSDB; AAT90472.
XX Nucleotide sequences encoding human agrin and muscle specific kinase
PT and related receptor - used in diagnosis and treatment of disorder
PT with muscle atrophy
XX Example 1; Fig 1; 120pp; English.
PS This polypeptide comprise a novel rat receptor tyrosine kinase
XX designated muscle specific kinase (MusK) that is expressed in
CC normal and denervated muscle. MusK is alternatively referred to
CC Dmk for denervated muscle kinase. The amino acid sequence was
CC deduced from an isolated cDNA clone (see AAT90472). Human MusK (see
CC AAW26611) has also been identified. Use of MusK to generate anti-
CC MusK antibodies and in the diagnosis of neurological or other
CC disorders is disclosed. Assay systems that may be used to detect
CC and/or measure ligands that bind the musk gene product are provided.
CC A claimed method of promoting the growth, differentiation or
CC survival of MusK receptor-expressing cells involves administration
CC to the cell of agrin (see AAW26609). Such cells include muscle,
CC heart, spleen, ovary and retina cells, or cells genetically
CC engineered to express the MusK receptor.
XX
SQ Sequence 868 AA;

Query Match 93.9%; Score 4292.5; DB 18; Length 868;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;
OY 1 MRELVINPLVHLLTVAFSGTEKLPKAPVITTPLETVDAIVEEATFMCAYESPOPEIS 60
Db 1 MRELVINPLVHLLTVAFSGTEKLPKAPVITTPLETVDAIVEEATFMCAYESPOPEIS 60
OY 61 WTRNKILIKLEFDRYSRENGOLITLISVEDSDGYCCANNGVGAIVSCGALQYKMK 120
Db 61 WTRNKILIKLEFDRYSRENGOLITLISVEDSDGYCCANNGVGAIVSCGALQYKMK 120
OY 121 PKITRPPINVKITIEGKAVLPCTTGNPKPSVSMIGDSPLRNSRIAYLESGLRIHNY 180
Db 121 PKITRPPINVKITIEGKAVLPCTTGNPKPSVSMIGDSPLRNSRIAYLESGLRIHNY 180
OY 181 OKEDAOQYRCVAKNSLGTAYSKVYKLEFEYFAITLAPESHNVTFSSVTLLHCTATGIPY 240
Db 181 OKEDAOQYRCVAKNSLGTAYSKVYKLEFEYFAITLAPESHNVTFSSVTLLHCTATGIPY 240
OY 241 PTTTMIENGNAVSSGSIQESVDRVIDSRLOLITTPGTYCTATKKGKSTAAAAAT 300
Db 241 PTTTMIENGNAVSSGSIQESVDRVIDSRLOLITTPGTYCTATKKGKSTAAAAAT 300
OY 301 ISTAEMSKPOKDKNGYCAQYRGECNAVLAKDALVELNTSYADPEBAOELLVHTANNEK 360
Db 301 ISTAEMSKPOKDKNGYCAQYRGECNAVLAKDALVELNTSYADPEBAOELLVHTANNEK 360
OY 361 VVSPVCRPAEALCNHIOECSRGVVPPIPCREYCAVKKLFEAKKELVNEETKNG 420
Db 361 VVSPVCRPAEALCNHIOECSRGVVPPIPCREYCAVKKLFEAKKELVNEETKNG 420
OY 421 LKSEMHLLSVPKSKLPSHMDPTACARLPHLDYKNENLKTPEPMTSKPSVDIPNLPS 480
Db 421 LKSEMHLLSVPECKSLPSHMDPTACARLPHLDYKNENLKTPEPMTSKPSVDIPNLPS 480
OY 481 SSSSSFSVSPYSMTVYIISMSFAIFVLLTTITLTCRRRKQWKKKRESAAVLTTLTP 540
Db 481 SSSSSFSVSPYSMTVYIISMSFAIFVLLTTITLTCRRRKQWKKKRESAAVLTTLTP 540
OY 541 SELLDRLHPNPMYQRMPLLNPKLLSLLEYPRNIEYVRDIEGAGRGVQARAPGLLPY 600
Db 541 SELLDRLHPNPMYQRMPLLNPKLLSLLEYPRNIEYVRDIEGAGRGVQARAPGLLPY 600
OY 601 EPTTMAVAVKMLKEASADQADFOREALMAEFDNPNIYKLLGVCAVGKPMCLLFEXMAY 660
Db 601 EPTTMAVAVKMLKEASADQADFOREALMAEFDNPNIYKLLGVCAVGKPMCLLFEXMAY 660

QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPPGPPPLSCAEOLCIAROVAAGMAYLSERK 720
DB 660 gdlneflrsmshphtvcslshtsdlsrarvsspppplscaeqlciarvaagmaylserk 719
QY 721 FVHRDLATRNCLVGENMNVYKIADFGLSRNISADYYKANENDAIPIRMMPESIFRYNYT 780
DB 720 fvhrdlatrnclvgenmvvkiadfglsrnlvsadykdgndaiplrmpesifrynytc 779
QY 781 TESDVWAGVGVLMWEIFSYGLOPYGYMAHEEVIYVRDGNILSCPENCPVELYNNMRLCWS 840
DB 780 tesdvwagvgvlmwelfsyglpygymahoevliyvrldgnllacpencpvelynlmrlcws 839
QY 841 KLPA DRPSFTSIRILERMCE RAGTVSV 869
DB 840 klpadrpsfcsihrlqrmceraegtvsv 868

RESULT 6
AAM26507 standard; protein; 868 AA.
AAM26507;
06-JAN-1998 (first entry)
Rat Dmk receptor.
Dmk receptor; tyrosine kinase receptor; signal transduction; assay;
therapy; diagnosis.
Rattus sp.
Key Location/Qualifiers
peptide 1..19
FT /label= Sig_peptide
FT Domain 20..492
FT /label= Extracellular
FT Domain 492..521
FT /label= Transmembrane
FT Domain 522..868
FT /label= Intracellular

XX US656473-A.
XX 12-AUG-1997.
XX 21-JUL-1993; 93US-0095658.
XX 19-JAN-1995; 95US-0374834.
XX 21-JUL-1993; 93US-0095658.
XX (REG-) REGENERON PHARM INC.
XX Rojas EA, Valenzuela DM;
XX WPI: 1997-414593/38.
XX N-PSDB: AAT87074.
XX New isolated human denervated muscle kinase receptor - used to
XX develop products for the diagnosis and treatment of neurological,
XX muscle or neuromuscular disorders
XX
XX Example 1; Column 19-24; 31pp; English.
XX This polypeptide sequence comprises the rat Dmk receptor, a novel
XX tyrosine kinase receptor that is expressed at high levels in an
XX denervated muscle. Its amino acid sequence was deduced from an
XX isolated cDNA clone (see AAT87074). Human Dmk receptor (see
XX AAM26506) has also been identified and human Dmk receptor (see
XX products for the diagnosis and treatment of neurological, muscle
XX or neuromuscular disorders.

SO Sequence 868 AA:
Query Match 93.9%; Score 4292.5; DB 18; Length 868;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;
QY 1 MRELVINPIPLVHILVAFSGTEKLPKAPVITPTPLEVDALVEEVPFMAVESYPOPEIS 60
DB 1 mrelvinppllgmltlvafsfgtelkpkapvltptplevdalveevpfmavesypopeis 60
QY 61 WTRNKILIKLPDRYSIRENGQILITLSEDSDDGICCTANNGVGAVSCGMLQYKMK 120
DB 61 wtrnkililiklpdrysirengqililtsevedsdgicyctanngvgavscgmlqykmk 120
QY 121 PKITRPPINVKIIEGLKAVIPCTTMGNPKPSVSWIKGDSPLRESRVAVESGLRIHNV 180
DB 121 pkitrppinvkiliegllkavipcttmgnpkpsvswikgdsalrestrlavlesgslrihmv 180
QY 181 QKEDAGYRCVAKNSLGTAVSKVYKLEFEYFARILRAPESHNTFGSPVTLHCTATGIPV 240
DB 181 qkedaggyrcvaknslgtavskvylefeyfarilrapeshntfgspvtlhcrtatgipv 240
QY 241 PPTWINGNAVSGSIOESYKDRVIDSRLOLFTTKGCLTCTTNHGEKFTAKAAT 300
DB 241 pttwingnavsgsioesykdrvidsrloqlfttkgcltcttnhgekfstaakaat 300
QY 301 ISTAEMSKPOKDNKGYCAOYRGECVGNALAKDALVFNTSYADPEAEQELVHTAMNKLK 360
DB 301 istaemskpdknkgycayrgecvgnalvkdalvfnltsyadpeaeqellvhtamnelk 360
QY 361 VVSPVCRPAEALLCNHIFECSPGVVPTPIPCREYCLAVKELFCAKEMLVMEKTHRG 420
DB 361 vvspvcrpaeeallcnhifecspgvvptpipecreyclavkelfcakemlvmeekthrg 420
QY 421 LYRSEMLLSVPRKSKLPSMHWMDPTACARLPHULYNNENKTFPPMSSKRVDPILPS 480
DB 421 lyrsesmlslsvprksklpsmhwmdptacarlphulynnenktfppmsskrvdpilps 480
QY 481 SSSSFVSVPYYSMTVLIISMSFAIFVLITITLYCCRRKQKNNKRESAAVTLTLP 540
DB 480 ssssfvsvpyysmtvliismsfaifvlititlyccrrrkqknnkresaaavltp 540
QY 541 SELLLDLRLHPNMYQRMPLINPKLSLEYPRNNIEYVDIGEGAFGRVQARPGLLPY 600
DB 541 sellldlrlhpnmyqrmpllnpklsleyprnnieyvdigegafgrvqarpgllpy 600
QY 601 EFFTMAVYKMKKEASADMOMDROREALMAEPNPNVYKLGCAVGKPMCLFEYWAY 660
DB 601 efftmayvymkkekassadmomdrorealmepnnpnyklgcavgkpmclfeymay 660
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPPGPPPLSCAEOLCIAROVAAGMAYLSERK 720
DB 660 gdlneflrsmshphtvcslshtsdlsrarvsspppplscaeqlciarvaagmaylserk 719
QY 721 FVHRDLATRNCLVGENMNVYKIADFGLSRNISADYYKANENDAIPIRMMPESIFRYNYT 780
DB 720 fvhrdlatrnclvgenmvvkiadfglsrnlvsadykdgndaiplrmpesifrynytc 779
QY 781 TESDVWAGVGVLMWEIFSYGLOPYGYMAHEEVIYVRDGNILSCPENCPVELYNNMRLCWS 840
DB 780 tesdvwagvgvlmwelfsyglpygymahoevliyvrldgnllacpencpvelynlmrlcws 839
QY 841 KLPA DRPSFTSIRILERMCE RAGTVSV 869
DB 840 klpadrpsfcsihrlqrmceraegtvsv 868

RESULT 7
AAR92717 standard; protein; 868 AA.
AAR92717;
AAR92717;

XX	27-MAY-1996	(first entry)
DT		
XX	Mouse muscle-localised protein-tyrosine-kinase receptor-2 isoform.	
XX		
DE		
XX	Mouse muscle-localised protein-tyrosine-kinase receptor-2 isoform;	
KW	mlk-2; treatment; monoclonal antibody; receptor ligand;	
KW	receptor;antagonist; muscular dystrophy; familial dysautonomia;	
KV	congenital myopathy; myotonia congenita; myasthenia gravis;	
KW	familial periodic paralysis; Eaton-Lambert syndrome;	
KW	paresis/smell myoglobinuria; secondary myasthenia;	
KW	dysregulation atrophy; nervous system disease; vascular disorder;	
KW	tremor; metabolic derangement; multiple sclerosis; epilepsy;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's chorea;	
KW	amyotrophic lateral sclerosis; primary lateral sclerosis;	
KX	Weednig-Hoffman disease; syringomyelia; peripheral neuropathy;	
KX	congenital anomaly; tumor.	
OS		
XX	Mus musculus.	
FH		
FH	Location/Qualifiers	
FT	Peptide	1..21
FT	/note-"mlk-2 protein signal peptide"	22..462
FT	/note-"soluble mlk-2 domain"	22..494
FT	Domain	22..494
FT	/note-"soluble mlk-2 domain"	22..494
FT	Domain	/note-"mlk-2 protein extracellular domain"
FT	Domain	495..515
FT	Domain	/note-"mlk-2 protein transmembrane domain"
FT	Domain	516..868
FT	Domain	/note-"mlk-2 protein intracellular domain"
FT	Domain	580..855
FT	/note-"mlk-2 protein-tyrosine-kinase domain"	
PN		
XX	WO9602644-A1.	
PD		
XX	01-FEB-1996.	
PE	06-JUL-1995;	95WO-US08493.
PR	01-FEB-1995;	95US-0384710.
PR	20-JUL-1994;	94US-0277803.
XX		
PA	(GEMV) GENETICS INST INC.	
XX		
XX	Carusio A, Wood C;	
DR	WIPI: 1996-105906/11.	
XX	N-PSSD; NANT16349.	
PT	DNA encoding 'muscle-localised kinase' family of receptor tyrosine	
PT	kinase(s) - also receptor ligands, antibodies and inhibitors,	
PT	useful for promoting or inhibiting bone or cartilage growth or bone	
PS	loss.	
PS		
PS	Claim 14; Page 71-73; 89pp; English.	
XX		
CC	Recombinantly produced mouse muscle-localised protein-tyrosine	
CC	-kinase receptor-2 isoform (mlk-2) may be used to identify and	
CC	isolate mlk-2 binding ligands, or to screen for agents capable of	
CC	binding to mlk-2 protein, which may act as inhibitors of normal	
CC	ligand binding. Isolated mlk-2 and mlk-2 receptor ligands may be	
CC	useful in the treatment of various medical conditions including:	
CC	muscle-related disorders, nervous system diseases, vascular	
CC	disorders, trauma, metabolic derangements, demyelinating diseases,	
CC	epilepsy, neuronal disease including motor neuron diseases,	
CC	syringomyelia, peripheral neuropathy, congenital anomalies and	
CC	tumours. Isolated mlk-2 protein may also be used to immunize	
CC	animals to obtain polyclonal and preferably monoclonal antibodies,	
CC	which specifically react with mlk-2 and which may inhibit ligand	
CC	binding to the receptor. These antibodies may be used as	

[illegible]

AAR92716
 ID AAR92716 standard; protein; 860 AA.
 XX
 AC AAR92716;
 XX
 DT 04-JUN-1996 (first entry)
 XX
 DE Mouse muscle-localised protein-tyrosine-kinase receptor-1 isoform.
 XX
 KW Mouse muscle-localised protein-tyrosine-kinase receptor-1 isoform;
 KW treatment; monoclonal antibody; receptor ligand;
 KW receptor-antagonist; muscular dystrophy; familial dysautonomia;
 KW congenital myopathy; myotonia congenita; myasthenia gravis;
 KW familial periodic paralysis; Eaton-Lambert syndrome;
 KW paroxysmal myoglobinuria; secondary myasthenia;
 KW denervation atrophy; nervous system disease; vascular disorder;
 KW trauma; metabolic derangement; multiple sclerosis; epilepsy;
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
 KW amyotrophic lateral sclerosis; primary lateral sclerosis;
 KW Meridig-Hoffman disease; syringomyelia; peripheral neuropathy;
 KW congenital anomaly; tumor.
 XX
 MS Mus musculus.
 XX
 Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "mlk-1 protein signal peptide"
 FT 22..453
 FT /note= "soluble mlk-1 domain"
 FT 22..486
 FT /note= "soluble mlk-1 domain"
 FT 22..486
 FT /note= "mlk-1 protein extracellular domain"
 FT 487..507
 FT /note= "mlk-1 protein transmembrane domain"
 FT 508..860
 FT /note= "mlk-1 protein intracellular domain"
 FT 572..847
 FT /note= "mlk-1 protein-tyrosine-kinase domain"
 XX
 PN W09602644-A1.
 XX
 PD 01-FEB-1996.
 XX
 PF 06-JUL-1995; 95WO-US08493.
 XX
 PR 01-FEB-1995; 95US-0384710.
 PR 20-JUL-1994; 94US-0277803.
 XX
 (GENY) GENETICS INST INC.
 PI Caruso A, Wood C;
 XX
 DR WPI; 1996-105906/11.
 DR N-PSDB; AAT16348.
 XX
 PT DNA encoding 'muscle-localised kinase' family of receptor tyrosine
 PT kinase(s) - also receptor ligands, antibodies and inhibitors,
 PT useful for promoting or inhibiting bone or cartilage growth or bone
 PT loss.
 XX
 PS Claim 14; Page 64-67; 89pp; English.
 XX
 CC Recombinantly produced mouse muscle-localised protein-tyrosine
 CC -kinase receptor-1 isoform (mlk-1) may be used to identify and
 CC isolate mlk-1 binding ligands, or to screen for agents capable of
 CC binding to mlk-1 protein, which may act as inhibitors of normal
 CC ligand binding. Isolated mlk-1 and mlk-1 receptor ligands may be
 CC useful in the treatment of various medical conditions including
 CC muscle-related disorders, nervous system diseases, vascular
 CC disorders, trauma, metabolic derangements, demyelinating diseases,
 CC epilepsy, neuronal disease, including motor neuron diseases,
 CC syringomyelia, peripheral neuropathy, congenital anomalies and

CC tumours. Isolated mlk-1 protein may also be used to immunize
 CC animals to obtain polyclonal and preferably monoclonal antibodies,
 CC which specifically react with mlk-1 and which may inhibit ligand
 CC binding to the receptor. These antibodies may be used as
 CC therapeutics for certain tumors and in the treatment of the above
 CC mentioned conditions. Smaller mlk fragments may be used to
 CC immunize animals.
 XX
 SQ Sequence 860 AA;
 Query Match 92.4%; Score 4220.5; DB 17; Length 860;
 Best Local Similarity 92.2%; Pred. No. 0;
 Matches 801; Conservative 29; Mismatches 30; Indels 9; Gaps 2;
 QY 1 MRELVIPLVHILTLVAFSGTEKPKRPVITTPLETYDALVEEATMCAVESYPOEIS 60
 DB 1 mrelvnpilqlmltlvafsfgtelkpkapvlttpletvdalveeatmcavesyppeis 60
 QY 61 WTRKKILIKLFDPFRYSIRENGQLTLTILSEBDDGICCTANNVGAVSCGALQYKMK 120
 DB 61 wttrnkliklfidfrysirengqltltlsvedsddgtycclannvgavscgalykkmk 120
 QY 121 PKITRPPINVKIIEGLKAVIPCTTGNPKPSVSWIKSDSPURENSRIAVLESGSLRTHNV 180
 DB 121 pkitrppinvklliegkavipcttgnpkspsvswikgdnalrensrlavlesgslrthnv 180
 QY 181 OKEDAGYRCVAKNSLTCTAASKVYKLEFEVFAIRLAPESHNVFGSFVTLHCATGIPV 240
 DB 181 qkedaagyrcvaknslctayskylvkleevfarllrpesunvfsgfvlrcataipv 240
 QY 241 PPTWIENGNAVSSGSIOESYKRVIDSRLQFLTKRGLYTCATNKGKFSATAKAAT 300
 DB 241 ptlswiengnavssgsiqesvkdtrvidsrldqfltkpglytcatnkhgkfstakaat 300
 QY 301 ISTAEKSPQKDNKGCAOTRGEVCNAVLAQDALVFINTSYADEPEAOELLHTANMEIK 360
 DB 301 istaewksqkdsqgycaqyrgvcdavlakdalvfintsyrdpeaqellihawelk 360
 QY 361 VVSPVCPRAAEALCNHIEFECSPGVVPTPIQRECLAVKELFCRKEWLVMEKTHRG 420
 DB 361 avspjcrpaaeallcnhlfgecspgvvptmpitrcyclavkelfckekwamegkhrq 420
 QY 421 LYRSEMLLSVPKCSKLPSMHWDEPTACARLPHLDYKNENLKTTPPMTSKPSVDIPMPS 480
 DB 421 lyrsghmllypvecsklpsmhwdptacarlphldyknenlktppmtskpsvdipnlp 471
 QY 481 SSSSEFSVSPYISMTVLIISMSFAIFVLTITTLVGCRRRKQKKNKRBSAATLTLP 540
 DB 472 astsfavspysmtvliisvstallaltlaltalcycrrtkewknkrrestavltcltp 531
 QY 541 SELLDRLHNPMTQRPMLLNPKLISLEYVRNNIEVDRIGEGAFGRVQARAGLLPY 600
 DB 532 sellldrlhnpmpyqrmpillnplklsleyvrnnieyvdrigegafgrvqaragllpy 591
 QY 601 EPTTMAVKMLKEBASDMQADFOREALAIAEPNPVITKILGVCAYGKPRCLLFETMAY 660
 DB 592 epttmavkmkleasadmqaadfgreaalmefdnphvkllygcavgykpmcllfeymay 651
 QY 661 GDINEFLRSMSPHRYCSLSHSDLSMRAOVSPGPPISCAEQLCIAOVAAGMAYLSERK 720
 DB 652 gdineflrsmphrvyslshtsdlsrtravsspppliscaeqclatqvaagmaylserk 711
 QY 721 FVHRDLATRNCLVGENNVKLIADGLSRNTYSADYYANENDALPIRMMPESIFYNRYT 780
 DB 712 fvhrdlatrncldvgennvkliadglsrnlysadyyanadgaadapirwmpesifynryt 771
 QY 781 TESQVMAVGVVLEIFESTGIOPYGMAHEEYIYVRGNILSCBENCPVELYNLMRCWS 840
 DB 772 tesqvavgvvlewelfestgiopygmaheeviyvrgnllacbenpvelynlmrlcws 831
 QY 841 KLPA DRPSFSIHRIERMCERAGTSVY 869
 DB 841 klpadrpsfshriermceragtsvy 869

Db	777	fynttcesdwagvylwelfsglppyygmahneeivyrldgnllacpenoplexnl	836
Oy	835	MLRCWSKLPADRPSTSIHRIILERMCEPRAECTVS	869
Db	837	mlrcwsklpadrpstfcsihrlilqmceraegtvy	871
RESULT 10			
AAW62568	standard; Protein; 871 AA.		
AAW62568; AAW62568;	12-Oct-1998 (first entry)		
DE	Mouse receptor tyrosine kinase Nsk2.		
XX	Nsk2; Msn-2; neural fold/somite kinase 2; receptor tyrosine kinase;		
KW	mouse; signal transduction; tumour; cancer; neuromuscular disease;		
KW	muscle; muscular dystrophy.		
XX	Mus sp.		
XX	Key	Location/Qualifiers	
FT	Peptide	1..21	
FT		/label= Sig_peptide	
FT		/note= "Claim 8"	
FT	Protein	22..871	
FT		/label= Mat_Protein	
FT	Region	22..496	
FT		/label= Extracellular	
FT		/note= "Claim 8"	
FT	Domain	49..98	
FT		/label= Ig_like	
FT		/note= "Claim 8"	
FT	Domain	233..282	
FT		/label= Ig_like	
FT		/note= "Claim 8"	
FT	Domain	401..450	
FT		/label= Ig_like	
FT		/note= "Claim 8"	
FT	Modified-site	222..224	
FT		/note= "Asn is N-glycosylated"	
FT	Modified-site	462..464	
FT		/note= "Asn is N-glycosylated"	
FT	Domain	497..517	
FT		/label= Transmembrane	
FT		/note= "Claim 8"	
FT	Region	518..871	
FT		/label= Intracellular	
FT		/note= "Claim 8"	
FT	Domain	518..576	
FT		/label= Juxtamembrane	
FT	Domain	577..858	
FT		/label= Tyrosine-kinase	
FT		/note= "Claim 8"	
FT	Domain	674..693	
FT		/label= kinase_insert	
FT		/note= "Claim 8"	
FT	Domain	859..871	
FT		/label= Carboxy-terminal	
FT		/note= "Claim 8"	
FT	Misc-difference	25	
FT		/note= "encoded by CcN"	
XX	WO9820114-A1.		
XX	14-MAY-1998.		
XX	29-OCT-1997;	97WO-US19646.	
XX	07-NOV-1996;	96US-0737855.	

Query Match	90.5%; Score 4136; DB 19; Length 871;
Best Local Similarity	90.3%; Pred. No. 0;
Matches 790; Conservative 30; Mismatches 45; Indels 10; Gaps	
QY 1 MRELVINIPVLHILTLVAFSGTEKLEPKAPVITTPLETVADLVEEATFMKAVSYROPETS 60	1 MRELVINIPVLHILTLVAFSGTEKLEPKAPVITTPLETVADLVEEATFMKAVSYROPETS 60
DB 1 mrelvniplilgmltlvafsgteklpkpviaplplevdalveevalfmavessypgels 60	1 mrelvniplilgmltlvafsgteklpkpviaplplevdalveevalfmavessypgels 60
QY 61 WTRNKKILKLPFTRPSIRENGQLTLTSLVEDSDDGICTANNNGVGAESGALQVKKK 120	61 WTRNKKILKLPFTRPSIRENGQLTLTSLVEDSDDGICTANNNGVGAESGALQVKKK 120
DB 61 wrnkkilklfptrpsirengqltlslvedsdgicciannngvgavessgalqvkkn 120	61 wrnkkilklfptrpsirengqltlslvedsdgicciannngvgavessgalqvkkn 120
QY 121 PKTRPPINVKLIIEGKAVLPCTMGNNPKPSYWKIGDSPLEKRSIRIAVESGSLRHNV 180	121 PKTRPPINVKLIIEGKAVLPCTMGNNPKPSYWKIGDSPLEKRSIRIAVESGSLRHNV 180
DB 121 pktrpplnvklieglkavlpctmgnpkpsyswlgdnalrensrialessgslrhnv 180	121 pktrpplnvklieglkavlpctmgnpkpsyswlgdnalrensrialessgslrhnv 180
QY 181 QKEDAGQRYCAVKAHNSLGTAYSKVYVLEPFVFRRIIRAPSHVNTRESFYLCTATGIVP 240	181 QKEDAGQRYCAVKAHNSLGTAYSKVYVLEPFVFRRIIRAPSHVNTRESFYLCTATGIVP 240
DB 181 qkedagqrycavkahnslgtayskvyvlepfvfrriirapshvntresfylvlctateigivp 240	181 qkedagqrycavkahnslgtayskvyvlepfvfrriirapshvntresfylvlctateigivp 240
QY 241 PTTWTIENNAVASGSIQESVYKDRVIDSLQFLFTPKGTYTICATNKHGEKSTAKNAAT 300	241 PTTWTIENNAVASGSIQESVYKDRVIDSLQFLFTPKGTYTICATNKHGEKSTAKNAAT 300
DB 241 ptlwtiengnavssgisiqesvdydrvidslqlfiktprgyltciatnkhgekstaknaat 300	241 ptlwtiengnavssgisiqesvdydrvidslqlfiktprgyltciatnkhgekstaknaat 300
QY 301 ISIAEMSKPQKDNKGCAQYRGEVCNAVY-----AKDALVFL-NTSYADPEEAQELLYHT 354	301 ISIAEMSKPQKDNKGCAQYRGEVCNAVY-----AKDALVFL-NTSYADPEEAQELLYHT 354
DB 301 vsiaemskpqkdnkgcaqyrgevcnavy-----gylmqpgpekmlivflptshrdpedagellint 357	301 vsiaemskpqkdnkgcaqyrgevcnavy-----gylmqpgpekmlivflptshrdpedagellint 357
QY 355 ANNELKAVSPVCPRAEALLCNHITQEGCGPVVPTPIPCRECYCLAVKLEFCAKEKLVM 414	355 ANNELKAVSPVCPRAEALLCNHITQEGCGPVVPTPIPCRECYCLAVKLEFCAKEKLVM 414
DB 358 annelkavspvcprraealclcnhitqegcgvvptpipcrcyclavklefcakeklvme 417	358 annelkavspvcprraealclcnhitqegcgvvptpipcrcyclavklefcakeklvme 417
QY 415 EKHTHGLYSEMHLLSVPCSKLPSHHMPTCARLPHLDYNNKENKTPTPTMSSPSVD 474	415 EKHTHGLYSEMHLLSVPCSKLPSHHMPTCARLPHLDYNNKENKTPTPTMSSPSVD 474
DB 418 gkhthgllyssmhlilpvpctrklpsmhndpctacturilyldykentltpstlsspsvd 477	418 gkhthgllyssmhlilpvpctrklpsmhndpctacturilyldykentltpstlsspsvd 477

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QY 475 IPNIPSSSSSFVSVPYISMTVIISMSFAIFVLLITTLTLCYCRRRKQKKNKRESAAV 534
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 ipnlp-satssfavspysmtvllsivslalfallclivclccrrrkewknkrestav 536
QY 535 TLTLPESELLDLRLHPWQRMPLLNPKLLSEYPRNNIEYRDIGEGAFGVFARA 594
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 537 cltlpseellldrlhprmpqrmpllnpkllseyprnnleyrdigegafigrvfgara 596
QY 595 PGLLPYEPFTMVAVKMLKEESADQMADFOREALMAEFDPNPVTKLIGCAVCKPKPCLL 654
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 597 pgllypepfcmvavkmlkeesasdmqdfgreaalmeefdnphlvklllycavqkpmcll 656
QY 655 PEYWAYDLDNEPLRSMSPHTVCSLSHSDLSMRAQVSSPGPPPLSCABQLCIARQVAAGMA 714
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 657 feymaygdlnelftrsmphvcslshedlstrarvsspgppplscacaeqlclarqvaagma 716
QY 715 YLSRKFVHRDLATRNCLVGENWVVKIADFGLSKNITISADYIKANENDALPIRMPEST 774
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QY 775 FYNRVTESDVMVAGVLMETFSYGLQPYGMAHEEYIYVRDGNILSCPCNPVELYNL 834
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QY 835 MRLCWSKLPADRPSEFSIHRLERMCERAGTYSV 869
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Db 837 mrlcwsklpadrpsfcshrlqgmceragetygv 871

RESULT 11
AAW62572 ID AAW62572 standard; Protein; 881 AA.
XX
XX AAW62572:
XX
DT 12-OCT-1998 (first entry)
XX
DE Mouse Nsk2 (alternatively spliced isoform).
XX
XX Nsk2; Nsn-2; neural fold/somite kinase 2; receptor tyrosine kinase;
KW mouse; signal transduction; tumour; cancer; neuromuscular disease;
XX muscle; muscular dystrophy.
XX
OS Mus sp.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /label= Sig-peptide
FT 22..871
FT /label= Mat-protein
FT Region 22..496
FT /label= Extracellular
FT Domain 49..98
FT /label= Ig-like
FT Domain 233..282
FT /label= Ig-like
FT Domain 401..450
FT /label= Ig-like
FT Modified-site 222..224
FT /note= "Asn is N-glycosylated"
FT Modified-site 462..464
FT /note= "Asn is N-glycosylated"
FT Domain 497..517
FT /label= Transmembrane
FT Region 518..881
FT /label= Intracellular
FT Domain 518..576
FT /label= Juxtamembrane
FT Domain 577..858
FT /label= Tyrosine-kinase
FT Domain 674..693
FT /label= Kinase_insert
FT Domain 859..881

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FT /label= Carboxy_terminal
XX
XX W09820114-A1.
PN
XX 14-MAY-1998.
PD
XX 29-OCT-1997; 97MO-US19646.
PF
XX 07-NOV-1996; 96US-0737855.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Reith A, Ruegg M;
PI
XX WPI; 1998-286930/25.
DR
XX
XX Muscle receptor tyrosine kinase, Nsk2, or its alternatively spliced
PT isoforms - useful for inhibiting receptor tyrosine kinase signalling
PT pathways and tumour development
XX
XX Claim 1; Fig 4b; 110pp; English.
PS
XX
XX This polypeptide comprises an isoform of a novel muscle receptor
CC tyrosine kinase (RTK) designated Nsk2 (neural fold/somite kinase)
CC (see also AAW62568) bearing an alternatively spliced C-terminal
CC domain (see also AAW62571). This isoform is produced in mouse foetal
CC myotube clones. Various alternative isoforms (see AAW62569-77) of Nsk2
CC have been identified that result from differential splicing of the
CC Nsk2 transcription unit. The invention provides expression vectors,
CC transformed or transfected host cells, a monoclonal antibody, a
CC related RTK designated Nsk1 (see AAV38551), and the following methods:
CC (a) screening for a neuromuscular disease (ND) by comparing the
CC levels of RTK from a sample and a control, where a difference is
CC indicative of ND; (b) monitoring the progression or regression of ND
CC by comparing the levels of RTK from a patient at different times, and
CC (c) determining the efficacy of a therapeutic agent in the treatment
CC of ND by comparing the levels of RTK prior to, and post-administration,
CC of the agent. The Nsk2 gene sequence can be used to study the growth
CC and differentiation of mammalian skeletal myotubes. Antibodies to
CC the protein are especially useful for inhibiting signal pathways
CC involving muscle RTks and thus can be used to inhibit tumour
CC development.
XX
XX Sequence 881 AA:
SQ
Query Match 90.3%; Score 4128; DB 19; Length 881;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 788; Conservative 30; Mismatches 44; Indels 10; Gaps 4;
QY 1 MRELVINPIVHILTLVAFSGTEKLPKAPVITPTPLEVDALIVEVATFMCAVESYPOPEIS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 mreivnpipllmlltvaifsteklppvylahplevdalveevatlmcavesyppeis 60
QY 61 WTRNKKILIRLFDTRYISIRENGQLLTLLSYEDSDDGICYCTANNVGVGAVESGALGVKMK 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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QY 121 PKTTRPPIVAKIIEGKAVLPCTTKMKNPKPSVSMIRGSDPLRENSKIANVLESGSLRIHW 180
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Db 121 pkttrppivakiiiegkavlpcttkmknppksvsmirgdsplrenskianvlesgslrihw 180
QY 181 OKEDAGQYRCVAKNSLGTAYSKVKVLEDFVFAIRILRAPSHNVTFGSFYTLICTATGIPV 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 qkedagqyrcvaknsigtatysklvkelevlgrllapeshnvtfgsfylctctelgipv 240
QY 241 PIIITWENGNAVSSGSIQDSVDRVIDYSRLQLEPTKPGLYTCIATANKHGEKFSYAKAAT 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 ptiswlngnavssgsiqdsivkdrvldsrllqflftkpglytclatnkhgekfstakaat 300
QY 301 ISIAEWSKPOKDKNGYCAQYRGECNAVLT-----AKDALVFL-NMSYADPEEAQELIVHT 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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FT	Region	514..867	/label="Intracellular
FT	Domain	514..572	/label="Juxtamembrane
FT	Domain	573..854	/label="Tyrosine-kinase
FT	Domain	670..689	/label="Kinase_Insert
FT	Domain	855..867	/label="Carboxy-terminal
PN	WO9820114-A1.		
PD	14-MAY-1998.		
XX	29-OCT-1997;	97WO-US19646.	
PF	07-NOV-1996;	96US-0737855.	
XX	(LUDW-) LUDWIG INST CANCER RES.		
PA	Reith A, Ruegg M;		
XX	WPI; 1998-286930/725.		
DR			
XX			
PT	Muscle receptor tyrosine kinase, Nsk2, or its alternatively spliced isoforms - useful for inhibiting receptor tyrosine kinase signalling pathways and tumour development		
PT			
XX			
PS	Disclosure; Page 68-70; 110pp: English.		
XX			
CC	This polypeptide comprises a novel muscle receptor tyrosine kinase (RTK) designated Nsk2 (neural fold/somite kinase) or Msn-2 that shows high sequence homology to Torpedo RTK. Various alternative isoforms (see AAW62568-77) of Nsk2 have been identified that result from differential splicing of the Nsk2 transcription unit. The CC invention provides expression vectors, transformed or transfected host cells, a monoclonal antibody, a related RTK designated Nsk1 (see AAW85551), and methods for screening for a neuromuscular disease (especially muscular dystrophy), monitoring the progression or regression of such a disease, and for testing the efficacy of therapeutic agents.		
CC			
CC			
CC			
SO	Sequence 867 AA;		
Query Match	90.1%; Score 4117; DB 19; Length 867;		
Best Local Similarity	90.2%; Pred. No. 0;		
Matches 786; Conservative % 30; Mismatches 45; Indels 10; Gaps 4;			
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DB	1 VNPILGLMTLVAISGTEKIPKPPVLAIPLETVALVEEATPFCVAVSYPQELISWRN 60		
QY	65 KILIKLEFDRYSIRENGOLITLSEVEDSDDIYCCFANNNGAVESGALQVMMKPKIT 124		
DB	61 KILIKLIFDYSIRENGOLITLSEVEDSDDIYCCFANNNGAVESGALQVMMKPKIT 120		
QY	125 REPINVKIIEELKAVLPCTTGNKRPYSWKGSPLRENSRIAVLESGLRIHNVOKED 184		
DB	121 RPIINVKIIEELKAVLPCTTGNKRPYSWKGSPLRENSRIAVLESGLRIHNVOKED 180		
QY	185 AGOIRCAVAKNSLIGTAVSVVWLEFEFVRRIIRAPESHVNTGSEVTLHCTATGIPVPIIT 244		
DB	181 AGQIRCAVAKNSLIGTAVSVVWLEFEFVRRIIRAPESHVNTGSEVTLHCTATGIPVPIIT 240		
QY	245 WIENGNVSSGSIQESVKKDRVIDSRLOLEFTRKPLDYTCIATNKGKRFSTAKAATISIA 304		
DB	241 WIENGNVSSGSIQESVKKDRVIDSRLOLEFTRKPLDYTCIATNKGKRFSTAKAATISIA 300		


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OY 305 EMSKPOKNGCYCAQYRGEVCNAVLT-----AKDALVFL-NTSYADPEBAOELLYVTAMNE 358
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OY 359 LKVVSPVCPAAEALLCNHIFQECSPGVVPTPIPICREYCLAVKELFCAKEMLVMEKTH 418
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Db 358 lkavspclptpaaellcyhlflcespyvvpmpmpcreyclavkelfcakewamegkah 417
OY 419 RGLVSEKHLISVPCSKLPSGMHMDPTACARLPHIDYKEMKTKPPPTSSKPSVDINL 478
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Db 418 rglvsgmhllyppecrklpsmhdpctactrlpyldykemkltcltprstssrpsadlpnl 477
OY 479 PSSSSSSFSVSPYMTYIISIMSFALFVLITFTLVCCRRKQWKKKRESAVTLTT 538
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Db 478 p-aastsfavpaymtvlstsvsalfalltlylccrrrkemkktrestavtlct 536
OY 539 LPSELLDLRHPNMYQKPLLNPKLISLEYPRNNIEYVDIGEGAFGRVQARAPGL 598
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Db 537 lpsellldrlhpnmyqmppllnpkllsteyprnnieyvdigegafgrvfgarapgl 596
/ 599 PYEPTMAVVMKLEKESADMDQADQREARALMAEPDNINIKLIGVCAGVGMCLLEFYM 658
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 597 pyeptmavvmklkeesadmdqadfqreaalmaetdnprnlvgcavgkpmcllfeym 656
OY 659 AYGDINEFLRSKSPHTVCSLSHSDLSMRQVSSPGPPPLSCAEQCLIAROYAAGMAYLSE 718
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Db 657 aygdineflrsmphvtcsleshdsltrarvssppplscseqclarygaagmaylse 716
OY 719 RKFYRDLATRNCLVGENMVKIADFGLSRNTYSADYKANKANDAIPIRMPPESTFNR 778
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Db 717 rkfyrdlatrnclygenmvkldfiglsrntysadykandaiplrmppestfnyr 776
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Db 777 yttedwmaygvvleifsyglqpygmaheviyyvrdsnllacpencplelynlmlrc 836
OY 839 WSKLPADRPSTSIHRILERMCEAEGTVSV 869
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Db 837 wsklpadrpstsfshrilmceraeagtvgv 867

RESULT 14
AAM62569
ID AAM62569 standard; Protein; 863 AA.
XX
AC AAM62569;
XX
DT 12-OCT-1998 (first entry)
XX
ME Alternatively spliced mouse receptor tyrosine kinase Nsk2.
XX
KW Nsk2; Msn-2; neural fold/somite kinase 2; receptor tyrosine kinase;
KW mouse; signal transduction; tumour; cancer; neuromuscular disease;
KW muscle; muscular dystrophy.
XX
OS Mus sp.
XX
FH Key 1.21 Location/Qualifiers
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FT Region 22..488 /label= Mat_protein
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FT 142..190
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FT 233..282
FT /label= Ig_like
FT Modified-site 222..224
FT /note= "Asn is N-glycosylated"

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FT Domain 489..509
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FT Region 510..863
FT /label= Intracellular
FT Domain 510..568
FT /label= Juxtamembrane
FT Domain 569..850
FT /label= Tyrosine-kinase
FT Domain 666..685
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FT Domain 851..863
FT /label= Carboxy-terminal
FT Msc-difference 25
FT /note= "encoded by CCN"
FT
FT W09820114-A1.
FT
FT 14-MAY-1998.
FT
FT 29-OCT-1997; 97WO-US19646.
FT
FT 07-NOV-1996; 96US-0737855.
FT
FT (LUDW-) LUDWIG INST CANCER RES.
FT
FT Reith A, Ruegg M;
FT WPI: 1998-286930/25.
FT
FT Muscle receptor tyrosine kinase, Nsk2, or its alternatively spliced
FT isoforms - useful for inhibiting receptor tyrosine kinase signalling
FT pathways and tumour development
FT
FT Claim 7; Fig 3a; 110pp; English.
FT
FT This polypeptide comprises an alternatively spliced isoform of
FT a novel mouse muscle receptor tyrosine kinase (RTK) designated Nsk2
FT (neural fold/somite kinase) (see also AAM62568). Its amino acid
FT sequence was deduced from a mouse skeletal myotube cDNA clone.
FT A deletion of 24 nucleotides (1415-1438) of Nsk2 cDNA (see AAY38546)
FT results in replacement of aa457-465 of Nsk2 with a single alanine
FT residue. This isoform is expressed in foetal myoblasts and derived
FT myotubes. Various alternative isoforms (see AAM62569-77) of Nsk2
FT have been identified that result from differential splicing of the
FT Nsk2 transcription unit. The invention provides expression vectors,
FT transformed or transfected host cells, a monoclonal antibody, a
FT related RTK designated Nsk1 (see AAY38551), and the following methods:
FT (a) screening for a neuromuscular disease (ND) by comparing the
FT levels of RTK from a sample and a control, where a difference is
FT indicative of ND; (b) monitoring the progression or regression of ND
FT by comparing the levels of RTK from a patient at different times, and
FT (c) determining the efficacy of a therapeutic agent in the treatment
FT of ND by comparing the levels of RTK prior to, and post-administration,
FT of the agent. The Nsk2 gene sequence can be used to study the growth
FT and differentiation of mammalian skeletal myotubes. Antibodies to
FT the protein are especially useful for inhibiting signal pathways
FT involving muscle RTKs and thus can be used to inhibit tumour
FT development.
FT
FT Sequence 863 AA;
FT
FT Query Match 89.5%; Score 4087; DB 19; Length 863;
FT Best Local Similarity 89.6%; Pred. No. 0;
FT Matches 784; Conservative 29; Mismatches 44; Indels 18; Gaps 5;
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OY 61 WTRNKLILKLEFTRYSIRENGQLTIISVEDSDGIIYCTTANNGYGVGAVESGALQVYMK 120
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181	QKEDAOQYRCVAKVNSIGTGYISKYVWLEEFVFRILRAEESHNMFSGSVTLHCNATGIPV
181	qkedagqycvacknalgtcyaklvaleevgrllrpesnlnvfsgsvtlrccealipv
241	PTTTHLENNNAVSSGSIQDSVKNDRVIDSRLOLFTKPGLYTCIATNKGKPFSTAKAAAT
241	pttthleennnavssgsiqdsvknldrvidsrllqfltkpglyciatnkgkfstakaat
301	ISIAENSKPOKKNKGCAQYRGEEVCNAVLT-----AKDAVFL-NTSVADPEEAOELLVHT
301	vsiaensksqksgycaggyrge---gylimgpgekmllvflptctshnpedaqelllht
355	ANNEELKVSPPVCRPAEALLCNHIFQECSPGVPTPIPICREYLAWELEFCAKEWLME
358	awneelkvasppvcrpaeeallcyhlfiecsppgvptpicreylawelcfckewgme
415	EKTHRGLYSEMHNLISVPKCSKLPSPMHMDPACRILPHLDYKNKNLKTTPPMNKSRSVD
418	gkthrglysgmhlllpveecklpsmhdpacctrilpyl-----afpstsrspsad
475	IRLPSSSSSSTVSPTYSMTVIISIMSFALFYLLITTTLLYCCRRRKNKKNKRESAAV
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535	TTTTPLSELLDRLHPNMVOMRPLLNPKLISLEPRNTEYVROIGEGAFGRVQARA
529	tlctplselldrlhpnmygrmlllnpkllisleprnmeleyrtdigegaigrvqara
595	PGLLPEPPTVAVVVKLKEASADQADFQEAALMAEFDPNPIVKKLGVCAVGKPMCLL
589	pglllpepftlvavvkmllkeesaadmqadfgreaalmeafdnprlvkllgycavgkpmc11
655	FETMAVYCDLNEFLRSMSPHTVCSLSHSDLSRAQVSPGPPRLSCAOLCIATQVAAVNA
649	feymaygdlnelrsmphvtcslshedsrlrsvspprlscaeqclciatqvaaama
715	YLSEKKFVHRDLATRNCLVGENNVYKLNDFGLSNITYSADYKANENDAIPIRMPPESEI
709	ylsekkfvrhrlatrnclvgenmvvklndfglsnitysadylanendaiipirmppesi
775	FYNRTTESDVMAYGVVLMETFSYGLDPPRYGMAHEEVIYVVRGNTLISCENCPVELYLV
769	fynrvtcsdvmaygvvllmetfsgldpprygmaheeviyvvrngntliscenpcvelylv
835	MRLCSKLPADRPSEFTSHIRLERMCEPRACTGVSV
829	mrlcswklpadrpsefshirlermcepractgvsv

FT	Protein	22..863
FT	/label= Mat_protein	
FT	Region	22..468
FT	/label= Extracellular	
FT	Domain	49..98
FT	/label= Ig_like	
FT	Domain	142..190
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FT	Modified-site	222..224
FT	/note="Asn is N-glycosylated"	
FT	Domain	489..509
FT	/label= Transmembrane	
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FT	/label= Intracellular	
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FT	Domain	851..873
FT	/label= Carboxy_terminal	
PX	WO9820114-A1.	
XX	14-MAY-1998.	
PD	29-OCT-1997;	97WO-US19646.
XX	07-NOV-1996;	96US-0737855.
PR	(LUDM-) LUDWIG INST CANCER RES.	
XX	Retch A, Ruegg M;	
PI	WPI; 1998-286930/25.	
DR	Muscle receptor tyrosine kinase, Nsk2, or its alternatively spliced isoforms - useful for inhibiting receptor tyrosine kinase signalling pathways and tumour development	
PT	Claim 7; Fig 4c; 110pp; English.	
PS	This polypeptide comprises an alternatively spliced isoform of a novel mouse muscle receptor tyrosine kinase (RTK) designated Nsk2 (neural fold/somite kinase) (see also AAM62568). A deletion of 24 nucleotides (1415-1438) of Nsk2 cDNA (see AAV38546) results in replacement of aa457-465 of Nsk2 with a single alanine residue, while further alternative splicing alters the C-terminal sequence (see also W625710). This isoform is expressed in foetal myoblasts. Various alternative isoforms (see AAM62569-77) of Nsk2 have been identified that result from differential splicing of the Nsk2 transcription unit. The invention provides expression vectors, a transformed or transfected host cell, a monoclonal antibody, a related RTK designated Nsk1 (see AAV38551), and the following methods for: (a) screening for a neuromuscular disease (ND) by comparing the levels of RTK from a sample and a control, where a difference is indicative of ND; (b) monitoring the progression or regression of ND by comparing the levels of RTK from a patient at different times, and (c) determining the efficacy of a therapeutic agent in the treatment of ND by comparing the levels of RTK prior to, and post-administration, of the agent. Antibodies to the protein are useful for inhibiting signal pathways involving muscle RTKs and thus can be used to inhibit tumour development.	
CC	SQ / Sequence	873 AA;
XX	Query Match	89.3%; Score 4079; DB 19; Length 873;
XX	Best Local Similarity	89.7%; Pred. No. 0;
XX	Matches 782; Conservative	29; Mismatches 43; Indels 18; Gaps 5;

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Page 16

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Db	121	pktrppinvlikglkavlpcttmgnpkpsvswikgdnalrensrtalesqslilhuv	180
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QY	595	PGLIYEPFTWYAVKMLEEASADQAOFOREALMAEFDPNPNVKLIGVACAVKRPCLL	654
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QY	655	FERYMAVGDLENEFLRSMSPHYVCSLSHDLKMRADYSSFGPPPLSCAEOLCTARQVAAAMA	714
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QY	715	YLSERKEVYRDIATNCLNGEMMYVKIADFGLSTRYISADVYKKNENDAPAIIRMPPEESI	774
Db	709	ylserkfvmrdiatnclngelmmyvkidfgslstrlylsadykykadgndapirimppeesi	766
QY	775	FYNRYTSESDWAVGCVLMEJFSYGLQBYVGNMAHEEVIYVRDGNILSCPENCFVELYNT	834
Db	769	fynrytseSDwavgvvlweifsyglqbygnmahheeviyvrdgnillacpencfelynl	826
QY	835	MRLCWSKLPADRPSTSTHRIIRERCEBAEGR	866
Db	829	mrlcwsklpadrpsfcsihtrllqrmceaeagc	860

Search completed: August 16, 2002, 13:37:49
Job time: 109 sec

CC method uses a mutated PKR nucleic acid which comprises a modification
 CC to the intracellular and extracellular domains, or comprises a
 CC modification to the intracellular domain and excludes any nerve growth
 CC factor receptor(s) (NGFR). The method uses mutated PKR as a cell
 CC surface marker, and is useful for identifying genetically modified cells,
 CC especially immunoselection of transduced mammalian cells, and for
 CC identifying mammalian cells expressing a protein of interest. The
 CC genetically modified marked cells may be used in an autologous or
 CC allogeneic setting e.g. gene therapy for bone marrow transplants, graft
 CC facilitation or immune reconstitution.

CC Sequence 869 AA:

Query Match 100.0%; Score 4569; DB 22; Length 869;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRELVINPLVHLITVAFSGTEKLPKAVITPTLETVDALVEEATMCAVESYPOEIS 60
 1 mrelvinplvhlitvafsgtekpkavitptletvdalveeatmcavesypoeis 60
 61 WTRNKLILKLFDTYSIRENGQLTILSVESDDGIYCTANNGVGAVESGALGVKMK 120
 61 wtrnklilklfdtysirengqltilsvesddgiyctannvgavescgalgvkmk 120
 121 PKTRPPINVKIIEGLKVLPCCTMGNPKPSVSWINKDSPLRENSRIAVESGSLRHNV 180
 121 pktrppinvkiiiegkvlpcctmgnpkpsvswinkdsplrensrilavescslrhnv 180
 181 OKEDAGQYCVANKSLGTAISVYKLEFEVFAIRLAPRSHNVTFGSFTVLHCTATIPV 240
 181 okedagqyctvankslgtaisvyklefevfarilapreshnvtfgsftvlhctatipv 240
 241 PITWTENGNNAVSSGSIQESVKRIDSRLQPLTRPGTLCTATNNGEKFSRAKAAT 300
 241 pitwtengnnavssgsiqesvkridsrlqpltrpgtltctatnngekfsrakaat 300
 301 ISIAEMSKPOKDNKGYCAQYRGECVNAVLAKDALVEFNTSYADPEEQELLVTANNEIK 360
 301 isiaemskpokdnkgycaqyrgecvnavlakdalvefntsyadpeeellvtanneik 360
 361 VVSPVCRPAEALCHNITFOECSPPGVPPPTICREYCAVKELFCAKEMLVNEEKTHRG 420
 361 vvspvcrpaeealchnitfoecspgvpppticreycavkeelfcakemlvneekthrg 420
 421 IYRSEHMLISVPCSLPSMHNPTACARPHNDNKKENKTPTPTSSKAPVDIPNLS 480
 421 iyrehmlisvpcslpsmhnpacarpndnkkenktptptsskapvdipnlss 480
 481 SSSSSPVSPTYSMTYIISMSFAIFVLTITLYCCRRKONKNNKRSAAVTLTTP 540
 481 ssssspvsptysmtyiismsfaifvltitlyccrrkonknnkrsaaavtlttp 540
 541 SELLDLRLHPNMYQMPPLLNKLLSLEYRNNIETVNDIGGAFGRVQARAPILPY 600
 541 selldlrlhpnmyqmppllnkllsleyrnnietvndiggafgrvqarapilpy 600
 601 BEPTWAVVAKLKEEAGADQADFOREAAALMAEPDNINIKLLGVCAVGRMCLFEYMAV 660
 601 bepwtavvamlkeeagadqadforeaaalmaepdninikllgvcavglrmclfeymav 660
 661 GDNLNFKLSMSPHTVCSLSHSDLSMRAQVSSPGPPLSCAEOLCIRQVAGAYISEBK 720
 661 gdlnfnklsmsphvtcslishsdlsmraqvsspgpplscaeolcirqvagayisebk 720
 721 FVHKLALFRNCIVGENMVKIADFGLSRNIIYADYYKANENDAIPIRMAPPESIFNRYT 780
 721 fvhklalfrncivgenmvkiadfglsrniiyadyykanendaipirmappesifnryt 780
 781 TESDWAAGVTLMEFSTGLQYRYGAHEEVYVYVADGNILSCPENGEVELYNMFLCMS 840
 781 tesdwaagvvtlmefstglqyrygaheevyvyvadgnilscpengevelynmflcms 840

841 KLPADRPSTIRHILERMCEBAGTYSV 869
 841 klpadrpstirhilmcebagtysv 869

RESULT 3
 ID AAM26611
 AA AAM26611 standard; Protein; 869 AA.

XX AAM26611;

DT 27-JAN-1998. (first entry)

DE Human muscle-specific kinase (MUSK).

KW Receptor tyrosine kinase; muscle specific kinase; MUSK; Dmk; human.
 ligand; agrin; diagnosis; therapy.

OS Homo sapiens.

PN MO9721811-A2.

PD 19-JUN-1997.

PF 13-DEC-1996; 96MO-US20696.

PR 10-MAY-1996; 96US-0644271.

PK 15-DEC-1995; 95US-0008657.

PA (REGG-) REGENERON PHARM INC.

PI Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;

DR WPI; 1997-332783/30.

DT N-PSDB; AAT90473.

PT Nucleotide sequences encoding human agrin and muscle specific kinase
 and related receptor - used in diagnosis and treatment of disorder

PS with muscle atrophy

XX Example 4; Fig 4; 120pp; English.

CC This polypeptide comprise a novel human receptor tyrosine kinase
 CC designated muscle specific kinase (MUSK) that is expressed in
 CC normal and denervated muscle. MUSK is alternatively referred to
 CC Dmk for denervated muscle kinase. The amino acid sequence was
 CC deduced from an isolated cDNA clone (see AAT90471). Rat MUSK (see
 CC AAT96610) has also been identified. Use of MUSK to generate anti-
 CC MUSK antibodies and in the diagnosis of neurological or other
 CC disorders is disclosed. Assay systems that may be used to detect
 CC and/or measure ligands that bind the musk gene product are provided.
 CC A claimed method of promoting the growth, differentiation or
 CC survival of MUSK receptor-expressing cells involves administration
 CC to the cell of agrin (see AAT96609). Such cells include muscle,
 CC heart, spleen, ovary and retina cells, or cells genetically
 CC engineered to express the MUSK receptor.

XX Sequence 869 AA:

Query Match 99.8%; Score 4558; DB 18; Length 869;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MRELVINPLVHLITVAFSGTEKLPKAVITPTLETVDALVEEATMCAVESYPOEIS 60
 1 mrelvinplvhlitvafsgtekpkavitptletvdalveeatmcavesypoeis 60
 61 WTRNKLILKLFDTYSIRENGQLTILSVESDDGIYCTANNGVGAVESGALGVKMK 120
 61 wtrnklilklfdtysirengqltilsvesddgiyctannvgavescgalgvkmk 120


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QY 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSRIAVLESGSLRIHNV 180
DB 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSRIAVLESGSLRIHNV 180
QY 181 OKEDAGORCAVAKNSIGTAYSKVVKLEFEVFAIRILRAPESHNVTCSTYTLHCTATGIPV 240
DB 181 OKEDAGORCAVAKNSIGTAYSKVVKLEFEVFAIRILRAPESHNVTCSTYTLHCTATGIPV 240
QY 241 PTTWIENGNAVSSGSIQSVKDRVIDSRLOLFTKPGYTCIATNKKGKSTAKAAT 300
DB 241 PTTWIENGNAVSSGSIQSVKDRVIDSRLOLFTKPGYTCIATNKKGKSTAKAAT 300
QY 301 ISIAEKSPQDKNGCYCAQYRGEVCNAVLAKDALVFLNTSYADPEAOELVHTANNEIK 360
DB 301 ISIAEKSPQDKNGCYCAQYRGEVCNAVLAKDALVFLNTSYADPEAOELVHTANNEIK 360
QY 361 VVSPVCRPAAEALCNHIFGECSPGVVPTPIPCREYCLAVKELCAKEMLVMEKTHRG 420
DB 361 VVSPVCRPAAEALCNHIFGECSPGVVPTPIPCREYCLAVKELCAKEMLVMEKTHRG 420
QY 421 LYSEEMHLLSVKCSKLPKSMNDPTACARLPDLIDYKNENLTPPMTSKSPVDIPNLP 480
DB 421 LYSEEMHLLSVKCSKLPKSMNDPTACARLPDLIDYKNENLTPPMTSKSPVDIPNLP 480
QY 481 SSSSEFSVSPYMTVTISISISFAIFLITITITTCRRKKOMKKNKRESAAVTLTLP 540
DB 481 SSSSEFSVSPYMTVTISISISFAIFLITITITTCRRKKOMKKNKRESAAVTLTLP 540
QY 541 SELLDLRHPNPTQRMPLLNPLKLSLEYPRNNIEYRDIGEGAFGVFOBARAGILPY 600
DB 541 SELLDLRHPNPTQRMPLLNPLKLSLEYPRNNIEYRDIGEGAFGVFOBARAGILPY 600
QY 601 EPPFMVAVKMLKEKESADMDQDFORALMAEDNPNTIKLLGVCAVGPCKLLEFYWY 660
DB 601 EPPFMVAVKMLKEKESADMDQDFORALMAEDNPNTIKLLGVCAVGPCKLLEFYWY 660
QY 661 GDLEEFKRSMPHTVCSHSDLSMRQVSSPGRPPSCAOLCIARVAGMAVYSEBK 720
DB 661 GDLEEFKRSMPHTVCSHSDLSMRQVSSPGRPPSCAOLCIARVAGMAVYSEBK 720
QY 721 FVHRDLATRNCLVGENNVKIADEGLSRNIYSADYKANENDAPIRMMPESIFVNYRT 780
DB 721 FVHRDLATRNCLVGENNVKIADEGLSRNIYSADYKANENDAPIRMMPESIFVNYRT 780
QY 781 TESOVAVGVVLMETFSYGLQPYTGMAHEEYITVVRGNIISCENKPEVELYNMLCWS 840
DB 781 TESOVAVGVVLMETFSYGLQPYTGMAHEEYITVVRGNIISCENKPEVELYNMLCWS 840
QY 841 KLPADRPSTSIHRILERMCEKRAEFTVS 869
DB 841 KLPADRPSTSIHRILERMCEKRAEFTVS 869
QY 869 KLPADRPSTSIHRILERMCEKRAEFTVS 869
DB 869 KLPADRPSTSIHRILERMCEKRAEFTVS 869

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RESULT 4
AAW26506 standard; Protein; 869 AA.
AAW26506:

06-JAN-1998 (first entry)
Human Dmk receptor.
Dmk receptor: tyrosine kinase receptor; signal transduction; assay;
therapy; diagnosis; Alzheimer's disease; Parkinson's disease;
amyotrophic lateral sclerosis; Lou Gehrig's disease;
idiopathic torsion dystonia; muscle atrophy.
Homo sapiens.
US5656473-A.
12-ADG-1997.

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XX 21-JUL-1993: 93US-0095658.
XX 19-JAN-1995: 95US-0374834.
XX 21-JUL-1993: 93US-0095658.
XX (REG- ) REGENERON PHARM INC.
XX Rojas EA, Valenzuela DM;
XX NPI: 1997-414593/38.
XX N-PSDB: AAT87073.
XX New isolated human denervated muscle kinase receptor - used to
XX develop products for the diagnosis and treatment of neurological,
XX muscle or neuromuscular disorders
XX Claim 4: Column 31-36; 31pp; English.
XX This polypeptide comprises the human Dmk receptor (AAW26506), a novel
XX tyrosine kinase receptor that is expressed in high levels in
XX denervated muscle. Its amino acid sequence was deduced from an
XX isolated nucleic acid molecule (see AAT87073). The Dmk receptor can
XX be used to screen for agents that interact with Dmk. Agents that
XX bind to the receptor may mediate survival and differentiation in
XX cells naturally expressing the receptor, but may also confer survival
XX and proliferation when used to treat cells engineered to express the
XX receptor. Dmk receptor polypeptides and polynucleotides can also be
XX used for detecting aberrancies in the function or expression of the
XX receptor which may be used in the diagnosis of muscular or other
XX disorders. Manipulation of the receptor or agonists which bind this
XX receptor may be used to treat neurological diseases, diseases of
XX muscle or neuromuscular unit disorders, including Alzheimer's
XX disease, Parkinson's disease, amyotrophic lateral sclerosis (Lou
XX Gehrig's disease), idiopathic torsion dystonia and muscle atrophy.
XX The extracellular domain (ECD) of the receptor can be used to block
XX the binding of receptor to target cells. A receptorbody comprising
XX the ECD fused to a human Ig gamma-1 constant region is claimed.
XX Sequence 869 AA:
XX
XX Query Match 99.8%; Score 4558; DB 18; Length 869;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MRLVNIPLVHLITFAAGTEKLPKAPITTPLEVDALVEVAFKCAVESYPOPEIS 60
XX 1 MELVNIPLVHLITFAAGTEKLPKAPITTPLEVDALVEVAFKCAVESYPOPEIS 60
XX 61 WFNKILIKLFTYRSIRENGOLITLSEDSDDGIYCTTANNVGAVESGALOVKKM 120
XX 61 WFNKILIKLFTYRSIRENGOLITLSEDSDDGIYCTTANNVGAVESGALOVKKM 120
XX 61 WFNKILIKLFTYRSIRENGOLITLSEDSDDGIYCTTANNVGAVESGALOVKKM 120
XX 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSRIAVLESGSLRIHNV 180
XX 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSRIAVLESGSLRIHNV 180
XX 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSRIAVLESGSLRIHNV 180
XX 181 OKEDAGORCAVAKNSIGTAYSKVVKLEFEVFAIRILRAPESHNVTCSTYTLHCTATGIPV 240
XX 181 OKEDAGORCAVAKNSIGTAYSKVVKLEFEVFAIRILRAPESHNVTCSTYTLHCTATGIPV 240
XX 241 PTTWIENGNAVSSGSIQSVKDRVIDSRLOLFTKPGYTCIATNKKGKSTAKAAT 300
XX 241 PTTWIENGNAVSSGSIQSVKDRVIDSRLOLFTKPGYTCIATNKKGKSTAKAAT 300
XX 301 ISIAEKSPQDKNGCYCAQYRGEVCNAVLAKDALVFLNTSYADPEAOELVHTANNEIK 360
XX 301 ISIAEKSPQDKNGCYCAQYRGEVCNAVLAKDALVFLNTSYADPEAOELVHTANNEIK 360
XX 361 VVSPVCRPAAEALCNHIFGECSPGVVPTPIPCREYCLAVKELCAKEMLVMEKTHRG 420
XX 361 VVSPVCRPAAEALCNHIFGECSPGVVPTPIPCREYCLAVKELCAKEMLVMEKTHRG 420

```


QY 421 LYRSEMHLLSVKPKSLPDKMNDPACARLPHLDYKNENKATPEPMTSKPSVDIPNLS 480
 DB 421 LYRSEMHLLSVKPKSLPDKMNDPACARLPHLDYKNENKATPEPMTSKPSVDIPNLS 480
 QY 481 SSSSSFSVSPYMTVITISIMSSFAIFVLTITTLCCRRKKOKNNKRESAAVTLTLP 540
 DB 481 SSSSSFSVSPYMTVITISIMSSFAIFVLTITTLCCRRKKOKNNKRESAAVTLTLP 540
 QY 541 SELLDLRLHPNPKYQMPLLNPKLISLEYPRNNIEYVRDISEGAFGRVQARAPGLPY 600
 DB 541 SELLDLRLHPNPKYQMPLLNPKLISLEYPRNNIEYVRDISEGAFGRVQARAPGLPY 600
 QY 601 EPTTVAVAVKMLKEEASADMDQADQOREAALMAEPDNNITKLLGVCAVGRKPMCLLFEXMAY 660
 DB 601 EPTTVAVAVKMLKEEASADMDQADQOREAALMAEPDNNITKLLGVCAVGRKPMCLLFEXMAY 660
 QY 661 GDINELRLSKSPPTVCSLSHSDLSMRAOVSSPPPLSCSEOLCIANQVAAAGAAYSERK 720
 DB 661 GDINELRLSKSPPTVCSLSHSDLSMRAOVSSPPPLSCSEOLCIANQVAAAGAAYSERK 720
 QY 721 FVHRDLATNCLVGENMNVYRIADFGLSRNTYSADYKANENDAIPIRMMPESIFYNRYT 780
 DB 721 FVHRDLATNCLVGENMNVYRIADFGLSRNTYSADYKANENDAIPIRMMPESIFYNRYT 780
 QY 781 TESDVAVGVVLMIEFSYGIQPIYGNABHEVITYVRDGNITLSPENCPELYNLMLRCLWS 840
 DB 781 TESDVAVGVVLMIEFSYGIQPIYGNABHEVITYVRDGNITLSPENCPELYNLMLRCLWS 840
 QY 841 KLPADRPSTSHRILERNKCEAECTVSV 869
 DB 841 KLPADRPSTSHRILERNKCEAECTVSV 869
 RESULT 5
 ID AAM26610 standard; Protein: 868 AA.
 AC AAM26610;
 DT 27-JAN-1998 (first entry)
 DE Rat muscle-specific kinase (MUSK).
 KM Receptor tyrosine kinase; muscle specific kinase; MUSK; Dmk; rat;
 KW ligand; agrin; diagnosis; therapy.
 XS Rattus sp.
 Key Location/Qualifiers
 FT Peptide 1..19
 FT Domain /label- Sig_peptide 21..492
 FT Domain /label- Extracellular_domain 493..521
 FT Domain /label- Transmembrane_domain 522..868
 FT Domain /label- Intracellular_domain
 PN M09721811-A2.
 PD 19-JUN-1997.
 PF 13-DEC-1996; 96MO-0520696.
 PR 10-MAY-1996; 96US-0644271.
 PR 15-DEC-1995; 95US-0008657.
 XX (REGG-) REGENERON PHARM INC.
 PA Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;
 PI WPI; 1997-332783/30.

DR N-PSDB; AAT90472.
 XX Nucleotide sequences encoding human agrin and muscle specific kinase
 PT and related receptor - used in diagnosis and treatment of disorder
 PT with muscle atrophy
 XX Example 1; Fig 1; 120pp; English.
 CC This polypeptide comprise a novel rat receptor tyrosine kinase
 CC designated muscle specific kinase (MUSK) that is expressed in
 CC normal and denervated muscle. MUSK is alternatively referred to
 CC Dmk for denervated muscle kinase. The amino acid sequence was
 CC deduced from an isolated cDNA clone (see AAT90472). Human MUSK (see
 CC AAM26611) has also been identified. Use of MUSK to generate anti-
 CC MUSK antibodies and in the diagnosis of neurological or other
 CC disorders is disclosed. Assay systems that may be used to detect
 CC and/or measure ligands that bind the musk gene product are provided.
 CC A claimed method of promoting the growth, differentiation or
 CC survival of MUSK receptor-expressing cells involves administration
 CC to the cell of agrin (see AAM26609). Such cells include muscle,
 CC heart, spleen, ovary and retina cells, or cells genetically
 CC engineered to express the MUSK receptor.
 XX Sequence 868 AA;
 SQ
 Query Match 93.98; Score 4292.5; DB 18; Length 868;
 Best Local Similarity 93.2%; Pred. No. 0;
 Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;
 QY 1 MRELNIPLVHLITFVAVSGTEKLPKAVITPTEVAVLBEVATPMCAVDSYQPEIS 60
 DB 1 mrelnplvhlitfvaavgteklpkavitp tevatp mca vdsy qp eis 60
 QY 61 WTRNKILKLPDTRYSIRENQQLTILSVEDSDGIYCCITANNNGAVESGALQVWK 120
 DB 61 wtrnkilklp dtrys irenqql tilsvedsdgiyccit annngav esgalqv wk 120
 QY 121 PKTRPPINVKIIEGKAVLPCTTMGNPKSVSNKGDSPLENSRIAVLESGLRIHV 180
 DB 121 pktrppinvk iiegkavlp cttmgnpk svsnk gdspl ensriav les glri hv 180
 QY 121 PKTRPPINVKIIEGKAVLPCTTMGNPKSVSNKGDSPLENSRIAVLESGLRIHV 180
 DB 121 pktrppinvk iiegkavlp cttmgnpk svsnk gdspl ensriav les glri hv 180
 QY 181 QKEDAGQRCVAKNSLSTAISKVVKLEFEVPAIRLPESHNVTFGSGVTLACRATGPV 240
 DB 181 qkedagqrcv aknslsta iskvvkle fevpair lrpeshnv tfgsgv tlcra tgpv 240
 QY 181 qkedagqrcv aknslsta iskvvkle fevpair lrpeshnv tfgsgv tlcra tgpv 240
 DB 181 qkedagqrcv aknslsta iskvvkle fevpair lrpeshnv tfgsgv tlcra tgpv 240
 QY 241 PTIWINGNNAVSSGSIQESYKDRVIDSRQLFTTKPGLYTCIATNKGKSTAKAAT 300
 DB 241 pt iwin gnnav ss gsiq esykdr vidsr qlfttkpg lytcia t nkgk staka at 300
 QY 241 pt iwin gnnav ss gsiq esykdr vidsr qlfttkpg lytcia t nkgk staka at 300
 DB 241 pt iwin gnnav ss gsiq esykdr vidsr qlfttkpg lytcia t nkgk staka at 300
 QY 301 ISLWNSKPKQDNKGYCAQYRGECVNAVLAKDALVFINTSYADPEEAOELLVTRANNELEK 360
 DB 301 islw nskpk qdnkgy caqyrg ecvnav lakdal v fintsy adpee aoellv tra nnele k 360
 QY 301 islw nskpk qdnkgy caqyrg ecvnav lakdal v fintsy adpee aoellv tra nnele k 360
 DB 301 islw nskpk qdnkgy caqyrg ecvnav lakdal v fintsy adpee aoellv tra nnele k 360
 QY 361 VSPVYCPAAEALICNIIEFQESPGVVPRIPICREYLAVKELFCAKEMLVMEKTHRG 420
 DB 361 vspvy cpa aeal icniief qespgvv pr ipicre yla vkel fca kemlv mek thrg 420
 QY 361 vspvy cpa aeal icniief qespgvv pr ipicre yla vkel fca kemlv mek thrg 420
 DB 361 vspvy cpa aeal icniief qespgvv pr ipicre yla vkel fca kemlv mek thrg 420
 QY 421 LYRSEMHLLSVKPKSLPDKMNDPACARLPHLDYKNENKATPEPMTSKPSVDIPNLS 480
 DB 421 LYRSEMHLLSVKPKSLPDKMNDPACARLPHLDYKNENKATPEPMTSKPSVDIPNLS 480
 QY 481 SSSSSFSVSPYMTVITISIMSSFAIFVLTITTLCCRRKKOKNNKRESAAVTLTLP 540
 DB 481 SSSSSFSVSPYMTVITISIMSSFAIFVLTITTLCCRRKKOKNNKRESAAVTLTLP 540
 QY 541 SELLDLRLHPNPKYQMPLLNPKLISLEYPRNNIEYVRDISEGAFGRVQARAPGLPY 600
 DB 541 SELLDLRLHPNPKYQMPLLNPKLISLEYPRNNIEYVRDISEGAFGRVQARAPGLPY 600
 QY 601 EPTTVAVAVKMLKEEASADMDQADQOREAALMAEPDNNITKLLGVCAVGRKPMCLLFEXMAY 660
 DB 601 EPTTVAVAVKMLKEEASADMDQADQOREAALMAEPDNNITKLLGVCAVGRKPMCLLFEXMAY 660
 QY 661 GDINELRLSKSPPTVCSLSHSDLSMRAOVSSPPPLSCSEOLCIANQVAAAGAAYSERK 720
 DB 661 GDINELRLSKSPPTVCSLSHSDLSMRAOVSSPPPLSCSEOLCIANQVAAAGAAYSERK 720

OY 661 GDLEFLRSMSPHTVCSLSHSDLSMRAOVSSPPPLSCAEOCLARQVAAAGMAYLSERK 720
 DB 660 gdlneflrsmshphtvcslshtsdlsrarsvssppplscaeqclarqvaagmaylsesrk 719
 OY 721 FVHRDLATRNCLVGENMVKIADFGLSRNITVSADYKANKENDAPIRMPPESTIFYNRYT 780
 DB 720 fvhrdlatrnclvgenmvkiadfglsrnlvsadykagndaplrmppestifynryt 779
 OY 781 TESDVMAVGVLWMEIFSYGLOPYGMAHEVYIYVADGNILSCPENCPVELYNMLRCLWS 840
 DB 780 tesdvavgvvlwmeifsyglopygmaheeviyvrdgnllacpencpvelynmlrlcws 839
 OY 841 KLPADRPSTSIHRIILERMCCERAEGETVSV 869
 DB 840 klpadrpsfcsihrlilgrmceraegvtgsv 868

RESULT 6

AAW26507 standard; Protein; 868 AA.
 AAW26507;
 06-JAN-1998 (first entry)
 Rat Dmk receptor.
 Dmk receptor; tyrosine kinase receptor; signal transduction; assay;
 therapy; diagnosis.
 Rattus sp.

Location/Qualifiers
 1..19
 /label= Sig-peptide
 Domain 20..492
 /label= Extracellular
 Domain 492..521
 /label= Transmembrane
 Domain 522..868
 /label= Intracellular

US5656473-A.
 12-AUG-1997.
 21-JUL-1993; 93US-0095658.
 19-JAN-1995; 95US-0374834.
 21-JUL-1993; 93US-0095658.

(REGG-) REGENERON PHARM INC.
 Rojas EA, Valenzuela DM;
 WPI; 1997-414593/38.
 N-PSDB; AAT87074.

New isolated human denervated muscle kinase receptor - used to
 develop products for the diagnosis and treatment of neurological,
 muscle or neuromuscular disorders

Example 1; Column 19-24; 31pp; English.

This polypeptide sequence comprises the rat Dmk receptor, a novel
 tyrosine kinase receptor that is expressed at high levels in
 denervated muscle. Its amino acid sequence was deduced from an
 isolated cDNA clone (see AAT87074). Human Dmk receptor (see
 AAW26506) has also been identified and can be used to develop
 products for the diagnosis and treatment of neurological, muscle
 or neuromuscular disorders.

SQ Sequence 868 AA;

Query Match 93.9%; Score 4292.5; DB 18; Length 868;
 Best Local Similarity 93.2%; Pred. No. 0;
 Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

OY 1 MRELVINPIVHILTLVAFSGTEKLPKAPVITTPLETVDALVEEATPMCAVESYPOPEIS 60
 DB 1 mrelvinpilhltlvafsgteklpkapvittptletvdalveeatpmcavesypopeis 60
 OY 61 WTRNKILIKLFDRYSIRENGOLITLVEDSDDGITCCANNVGCAVESCGLAYKMK 120
 DB 61 wtrnkililikfdrysirengolltlsvedsddgityccannvgcavescglaykkm 120
 OY 121 PKITRPPINKIIEGLKAVLPCTTGNPKPSVSMIKDPSLRENSRAVLESGLRIHNV 180
 DB 121 pkitrppinkiiieglkavlpcttgnpkpsvsmikdpslrensravlesglrlhmv 180
 OY 181 QKEDAGYRCVANKSLGTAYSKVYKLEFEVFARILAPESHNVTFSSFVTLHCTANGIPV 240
 DB 181 qkedagyrccvankslgtayskvylkefevfarilapeshnvtfssfvrtlctangipv 240
 OY 241 PTTTWIENGNAVSSGSIQESVDRVIDSRLOLEITPKGYTCIATKHKKESTAKAAAT 300
 DB 241 pttwiengnavssgsiqesvdrvidsrloletpkgytciatkhhkestakaaat 300
 OY 301 ISTAEKSKQKKNKGCAQYRGECNAVLAKDALVELNTSYADPEBAQELVTANNELK 360
 DB 301 istaekskqkknkgcaqyrgevcnavlakkdalvelntsyadpebaqelvtannelk 360
 OY 361 VVSPVCRPAEALCNHIEQECSPGVPPPIPCREYCAVEMLPKAKMLVKEETHRG 420
 DB 361 vvspvcrpaecalcnhieqecspgvpppipcreycavemlpkakmlvkeethrg 420
 OY 421 KYRSEMHLSVPCSKSLSMHMDPTFACARPLHDYKNENLTFPPMTSSKPSVDIPNLS 480
 DB 421 kyrsemhlsvpcskslsmhmdptfacarplhdyknenltpfpmstsskpsvdipnls 480
 OY 481 SSSSFSVSPRTSMVTIISIMSSFAIFVLITTTIXCCRRKQKKNKRESAAVTLTLP 540
 DB 481 ssssfsvsprrtsmvtiisimssfaifvlitttixccrrkqkknkresaaavtltlp 540
 OY 540 astsfavspysmtvllismcfaifaliltltyccrrrremkkrresaavtltlp 539
 OY 541 SELLDRLHPNMQRMELLPKLLSLDEYPRNNIEYVADIGEGAFGRVFOARAGLLPY 600
 DB 541 selldrlhpnmqrmellpkllsldeyprnnieyvadigegafgrvfoaragllpy 600
 OY 601 EPTWVAVKMLKEEASADMOMDFOREALMAEFDPNIVKLLGVCAVGRPKCLTEYNAY 660
 DB 601 eptwvavkmlkeeeasadmomdforealmaefdpnivkllgvcavgkpmcllteynay 659
 OY 661 GDLEFLRSMSPHTVCSLSHSDLSMRAOVSSPPPLSCAEOCLARQVAAAGMAYLSERK 720
 DB 660 gdlneflrsmshphtvcslshtsdlsrarsvssppplscaeqclarqvaagmaylsesrk 719
 OY 721 FVHRDLATRNCLVGENMVKIADFGLSRNITVSADYKANKENDAPIRMPPESTIFYNRYT 780
 DB 720 fvhrdlatrnclvgenmvkiadfglsrnlvsadykagndaplrmppestifynryt 779
 OY 781 TESDVMAVGVLWMEIFSYGLOPYGMAHEVYIYVADGNILSCPENCPVELYNMLRCLWS 840
 DB 780 tesdvavgvvlwmeifsyglopygmaheeviyvrdgnllacpencpvelynmlrlcws 839
 OY 841 KLPADRPSTSIHRIILERMCCERAEGETVSV 869
 DB 840 klpadrpsfcsihrlilgrmceraegvtgsv 868

RESULT 7

AAW26507 standard; Protein; 868 AA.
 AAW26507;
 06-JAN-1998 (first entry)
 Rat Dmk receptor.
 Dmk receptor; tyrosine kinase receptor; signal transduction; assay;
 therapy; diagnosis.
 Rattus sp.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2002, 13:36:00 ; Search time 15.06 seconds

(without alignments)
2234.216 Million cell updates/sec

Title: US-09-817-487a-2

Perfect score: 4569

Sequence: 1 MRRLVNIPLVHILTVAFSG.....TSIHRIILRCMCAEGTVSV 869

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	906.5	19.8	937	1	ROR1_MOUSE
2	899	19.7	937	1	ROR1_HUMAN
3	886.5	19.4	944	1	ROR2_MOUSE
4	876	19.2	943	1	ROR2_HUMAN
5	862	18.9	821	1	TRKB_MOUSE
6	861	18.8	822	1	TRKB_HUMAN
7	858	18.8	818	1	TRKB_MOUSE
8	854.5	18.7	1051	1	TRKB_RAT
9	833	18.2	1051	1	PRK7_MOUSE
10	813	17.8	827	1	TRKC_MOUSE
11	812	17.8	796	1	TRKA_MOUSE
12	792.5	17.3	839	1	TRKC_HUMAN
13	788.5	17.3	825	1	TRKC_MOUSE
14	781.5	17.1	799	1	TRKA_RAT
15	774	16.9	1070	1	PRK7_HUMAN
16	768	16.8	864	1	TRKC_RAT
17	751	16.4	778	1	TRKA_MOUSE
18	706	15.5	806	1	CEK2_MOUSE
19	703.5	15.4	801	1	CEK2_HUMAN
20	702	15.4	801	1	CEK3_MOUSE
21	701	15.3	806	1	CEK3_MOUSE
22	698.5	15.3	802	1	CEK3_MOUSE
23	693.5	15.2	802	1	CEK3_MOUSE
24	683	14.9	821	1	CEK3_MOUSE
25	677	14.8	822	1	CEK3_MOUSE
26	675.5	14.8	808	1	CEK3_MOUSE
27	675	14.8	808	1	CEK3_MOUSE
28	675	14.8	808	1	CEK3_MOUSE
29	675	14.8	808	1	CEK3_MOUSE
30	671.5	14.7	822	1	CEK3_MOUSE
31	669	14.6	822	1	CEK3_MOUSE
32	669	14.6	822	1	CEK3_MOUSE
33	667	14.6	822	1	CEK3_MOUSE

34	666.5	14.6	1333	1	VGRL_MOUSE
35	665	14.6	1382	1	INSR_HUMAN
36	663	14.5	1372	1	INSR_MOUSE
37	662.5	14.5	1363	1	ILPR_BRALA
38	662	14.5	890	1	TYO3_HUMAN
39	662	14.5	994	1	MEK_MOUSE
40	661.5	14.5	994	1	MEK_MOUSE
41	653.5	14.3	794	1	TRK1_MOUSE
42	653.5	14.3	1338	1	VGRL_HUMAN
43	651.5	14.3	640	1	IGIR_BOVIN
44	651.5	14.3	978	1	KEMS_RAT
45	651.5	14.3	1373	1	IGIR_MOUSE

ALIGNMENTS

```

RESULT 1
ID ROR1_MOUSE STANDARD: PRT: 937 AA.
AC Q92139.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor ROR1 precursor
DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1)
DE (ROR1).
GN ROR1 OR NTRKRL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99248426; PubMed=10231392;
RA Oishi T., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.,
RA Hattori T., Akita S., Matsuda Y., Yamamura H., Otsu H., Minami Y.;
RT "Spatially regulated expression of receptor tyrosine kinases,
RT mror1, mror2, during mouse development: implications in development
RT and function of the nervous system.";
RL Genes Cells 4:41-56(1999).
CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHOSE ROLE IS NOT YET
CC CLEAR.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE ROR SUBFAMILY.
CC
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB010383; BAA75480.1; -.
CC HSSP: P00747; ICEA.
CC MGD: MGI:1347520; Ror1.
CC InterPro: IPR000719; Euk_Pkinase.
CC InterPro: IPR000024; Fz_domain.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR01245; Tyr_Pkinase.
CC Pfam: PF01392; Fz; 1.
CC Pfam: PF00047; Ig; 1.
CC Pfam: PF00051; kringle; 1.
CC Pfam: PF00069; pkinase; 1.

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DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO0109; TYRKINASE.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00219; TYRC; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS00021; KRINGLE_1; FALSE_NEG.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR PROSITE; PS500107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
KM Immunoglobulin domain.
FT SIGNAL 1 29
FT CHAIN 30 937
FT DOMAIN 30 406 POTENTIAL.
FT TRANSMEM 407 427 TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT DOMAIN 428 937 RECEPTOR RORL.
FT DOMAIN 773 139 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 165 299 POTENTIAL.
FT DOMAIN 312 391 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 473 746 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 753 782 FZ.
FT DOMAIN 784 851 KRINGLE.
FT DOMAIN 853 876 PROTEIN KINASE.
FT N-BIND 479 487 SER/THR-RICH.
FT BINDING 506 506 ATP (BY SIMILARITY).
FT ACT_SITE 615 615 ATP (BY SIMILARITY).
FT MOD_RES 645 615 BY SIMILARITY.
FT DISULFID 79 131 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 937 AA; 104156 MW; D728733E67D1782C CRC64;

Query Match 19.88; Score 906.5; DB 1; Length 937;
Best Local Similarity 29.68; Pred. NO. 4.4e-53;
Matches 241; Conservative 106; Mismatches 253; Indels 215; Gaps 24;

QY 123 ITRPPIVKKIIEGLKAVLPCTTGNPKPSVWIKGDSPTRENSRI--AVLESGLRIH 178
DB 60 LDEPMNNTISLGGTAELHCKVSGNPPPSIRWFKNDAPVYGEPRISPRATNYGSRRLR 119
QY 179 NVOKEDAGQYRCVAKNSLGTAVSKVVKLEFEVFAKILRAPESHVNTGSEVTLHCTATGI 238
DB 120 NLDTTDTGYFQCVAATNG-----KKVYSTGYLF-----VKRG----- 151
QY 239 PVPITITMENGNNAVSSGSIQESVDRIYDRLQFLITKPGLYCIATNKHGEKFSKAA 298
DB 152 PPTI-----ASPSSDEYED----- 167
QY 299 ATISIAEMSKPQKDNKGYCAQYRGEVCNAVLAQDALVFLNTSYADPE-EAQELLVHTAMN 357
DB 168 -----GFCOPYRGIAAC-ARFIGNRTVMESLIHQGELENDITAFATWIG 210
QY 358 ELKVVSPVCRPAEALLCNHIEFGQC-SFGVYPTPIPCREKCLAVKELFCCKEMLVMEK 416
DB 211 TSSHLSQKCOFAIPSLCHYAFPYCDETSYVPRDLCRDCEVLNVLCOTEYI----- 265
QY 417 THRGLYKSE--MHLLSVKPSKSLPSMHMDPTA-CAR--LPHLDYKNENLTFP----- 464
DB 266 -----FANSNPILMKRIKIPNCEDELPPQSPPEANACIRIGIMADPINKNHKCYNSTGVDY 321
QY 465 -----PMTSKSPVDIPNL-----PSSSSS---FSVSFTY 492
DB 322 RGTAVSVTKSGHOCQPMNSQYPHTHSFTALRPELNGHSHYCRNPGNOKKEAPWCFTLDENF 381
QY 493 -----SMTVIISMSFAIPVLLITLITLITLTYCCORRRKQKNNKRRSAA 533

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DB 382 KSDLCDIPACDSKDSKKNKMEILYILVPSVALPLAIAELFFEICVCRNNQSS----- 435
QY 534 VLTITLPSSELLDRHPNMYORMP-----LLN---PKLSLEYPRNRIEYVD 580
DB 436 -----SPVQROPVPYGVQNEKMLNAYPKSKAKELPLSAVFME 478
QY 581 IGEAGRGVFOAR--APGLIPEPTMTVAVKMLKEBASADMDQADFOREALAAEDNPNI 638
DB 479 LGECTGKTIYKGLHYLPGM---DHAQLVAIKTLKDYNNPQOMTEFQOEASLAMELHPNI 535
QY 639 VLLGVCAVCKPMLCLPEYKAYADLNEPLRSMSPHNVCSLSLMSRAQVSPGPPLS 698
DB 536 VCLLGAVTQOPVCMPEFYNNQGLHFEFLMRSP-----HSDVCCSSDEDTGVSSSD 588
QY 699 CAEOLCIARQVAGMAVLSERKFEVHDLATRNCLVGENNVYKTADEGLSRNITYSADYKA 758
DB 589 HGFPLHAIQIAGMEYLSHFVHDLARNTLIEQLHVKISDGLSREIYSADYRV 648
QY 759 NENDAIPIRMPPESIFRNRYTTESDVMAVGVVLMETFGLOPYTGMAHEVIYVYRG 818
DB 649 QSKSLPIRMPPPEALMYGKFSSDSIWISGVVLMETFGLOPYTGFSNOEVIEMVRR 708
QY 819 NIISCPCNCEVELYNLMRLQMSKLPADPSESTIH 853
DB 709 QLLPCSEDCPPRMYSILMTBCEWNEIPSKRPKDIH 743

RESULT 2
RORL_HUMAN STANDARD; PRT; 937 AA.
ID RORL_HUMAN
AC 001973; Q92776;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor RORL precursor
DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1).
GN ROR1 OR NTRK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=93100347; PubMed=1334494;
RA Maslakowski P., Carroll R.D.;
RT "A novel family of cell surface receptors with tyrosine kinase-like
RT domain."
RT J. Biol. Chem. 267:26181-26190(1992).
RN [2]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=97030043; PubMed=8875995;
RA Reddy U.R., Phatak S., Pleasure D.;
RT "Human neural tissues express a truncated Ror1 receptor tyrosine
RT kinase, lacking both extracellular and transmembrane domains."
RT Oncogene 13:1555-1559(1996).
CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHOSE ROLE IS NOT YET
CC CLEAR.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM/T-ROR1; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN HUMAN HEART, LUNG, AND
CC KIDNEY, BUT WEAKLY IN THE CNS. THE SHORT ISOFORM IS STRONGLY
CC EXPRESSED IN FETAL AND ADULT CNS AND IN A VARIETY OF HUMAN
CC CANCERS, INCLUDING THOSE ORIGINATING FROM CNS OR PNS
CC NEUROECTODERM.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING EARLY
CC EMBRYONIC DEVELOPMENT. THE EXPRESSION LEVELS DROP STRONGLY AROUND
CC DAY 16 AND THERE ARE ONLY VERY LOW LEVELS IN ADULT TISSUES.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

```

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE ROR SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M97675; AAA60275.1; -;
 DR EMBL: U38894; AAC50714.1; -;
 DR HSSP: P00747; ICEA.
 DR MIM: P02336; -;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF01392; Fz; 1.
 DR Pfam: PF00047; Iq; 1.
 DR Pfam: PF00051; Kringle; 1.
 DR Pfam: PF00059; Kringle; 1.
 DR PRINTS: PR0018; Kringle.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00408; IGC2; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS50038; F2; 1.
 DR PROSITE: PS50021; KRINGLE_1; FALSE_NEG.
 DR PROSITE: PS50070; KRINGLE_2; 1.
 DR PROSITE: PS50107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50109; PROTEIN_KINASE_TYR; 1.
 DR Transmembrane: Tyrosine-protein kinase; ATP-binding; Receptor;
 DR Transmembrane: Signal; Glycoprotein; Kringle; phosphorylation;
 DR Immunoglobulin domain; Alternative splicing.
 DR SIGNAL 1 29
 FT CHAIN 30 937
 FT DOMAIN 30 406
 FT TRANSMEM 407 427
 FT DOMAIN 428 937
 FT DOMAIN 73 139
 FT DOMAIN 165 299
 FT DOMAIN 312 391
 FT DOMAIN 473 746
 FT DOMAIN 753 782
 FT DOMAIN 784 851
 FT DOMAIN 853 876
 FT NP_BIND 479 487
 FT BINDING 506 506
 FT ACT_SITE 615 615
 FT MOD_RES 645 645
 FT DISULFID 79 131
 FT CARBOHYD 47 47
 FT CARBOHYD 66 66
 FT CARBOHYD 184 184
 FT CARBOHYD 315 315
 FT VARSPPLIC 549 549
 FT SEQUENCE 937 AA: 104312 MW: 0D0694DBF2964773 CAC64;

Query Match 19.7%; Score 899; DB 1; Length 937;
 Best Local Similarity 31.5%; Pred. No. 1.4e-52;
 Matches 229; Conservative 102; Mismatches 254; Indels 142; Gaps 20;

OY 221 HAVT--FGSFVTLHCTATGTPPTTWINGNANVSGSIOESYKDRVIDSRQ---LFTT 275
 DB 65 NNTTSLGOTAEHLCKVSGNPPPTIMFKNDAPVVOEPRLSRSTIYGSRLRLRLDPT 124

OY 276 KPGVTCIATNKHGEKSTAKAATISTAEKSP-----QKNKGCAQYRGEVCAVLAK 331
 DB 125 DTGYFOVAINGKEVYSTGVLFVKFGPPPTASPGYSDEYDEDFCQYRGIAC-ARF IG 183
 OY 332 DALFVLTNTSYADPE-EAQQELLVHTAMNKLKVSPYCRPAABALLCNHIFQGC-SPGVVPT 389
 DB 184 NRTYVMSLHMOGELNENITAFNMGISLSLSDKCSQFALPSLCHVAFPCDETSYVK 243
 OY 390 PIPICREYCLAVKELFCAKKWLVEEKTGRGLYSE---MHLSVPCSKLPSMHMDPTA 446
 DB 244 PRDLRCRDECELLENVLCOTEYI-----FARSNPAILRLKLPNCEDLPQESPEEA 294
 OY 447 -CAR--LPHLIDYKNENKTE-----PPTSSKPSV----- 473
 DB 295 NCTIGLPMADPIKNKHCINSGVDYRGIVSYTKSGRQCQPMNSQYPRHTFTALRPE 354
 OY 474 -----LLIN---PKLLSLEYPRNTEYVRDIEGAFGRYEQAR--APGLLPPEPTMV 606
 DB 355 LINGHSYCRNPGNOKEAAPWCTLDENFKSDLCIDIPADSKSKRKN-----KMEILVIV 409
 OY 502 SSFAIFVLLITTYCCRRRKKOMKKRESAAVTLTTLPSELLRLHPNPMYQMP-- 558
 DB 410 PSVAIPALIALLEFFICVCR---NNOKSSAPV-----ORQPKHV 446
 OY 559 -----LLIN---PKLLSLEYPRNTEYVRDIEGAFGRYEQAR--APGLLPPEPTMV 606
 DB 447 RGVNVEKSMNLNAYKPKRAKELPLSAVRMEELDECAFGKTYKGLHYLPGR--DHAOLV 503
 OY 607 AVKMLKEASADQADQFQREALAEFDNPNTYKLLGCAVGRKPCLLFEYMAYGDLNEF 666
 DB 504 AIKTLKYNPQOMQWMEFOQESALMAELHNPVILLGAVQEQVCMLEFVINGDGLHEF 563
 OY 667 LRSMPHTVCSLSHSDSMRAQVSSPPPLSCAEQICIRQVAAAGAYISERFVARDL 726
 DB 564 LIRSP-----HSDVCGSSDEDEGYTKSSLDHGFHIALQIAGAEVYSSHEFVKDL 616
 OY 727 ATRNCLVGENMYKIADEGLSRNTYSADYYKANDNDPIRMPMPESIFYNRYTTESDVW 786
 DB 617 AARNILGLDHLVKISDLGLSREITYSADYRYVQSKSLPIRMPPEALMYGKSSDSIDV 676
 OY 787 AYGVLMEIFSYGLOPYGMAHEVITYYVDGNILSPENCPELVLYMLRLCKSLPADR 846
 DB 677 SFGVLMELTFSGLQPYGYGHFNDEIVEMVRKROLLPCSEDCPPMWSLMECWNELPSRR 736
 OY 847 PSEFTSH 853
 DB 737 PRFKDH 743

RESULT 3
 ROR2_MOUSE STANDARD; PRT; 944 AA.
 ID ROR2_MOUSE
 AC 092138;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor ROR2 precursor
 DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2)
 DE (ROR2).
 GN ROR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RX MEDLINE=99248426; PubMed=10231392;
 RA Oishi T., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.-J.,
 RA Hata T., Akira S., Matsumura Y., Yamamura H., Otani H., Minami Y.,
 RT Spatio-temporally regulated expression of receptor tyrosine kinases,
 RT mror1, mror2, during mouse development: implications in development
 and function of the nervous system.";
 RL Genes Cells 4:41-56(1999).

ID ROR2_HUMAN STANDARD: PRT: 943 AA.
 AC Q01974; Q9HAV7; Q9H861;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor ROR2 precursor
 DE (EC 2.7.1.112) (neurotrophic tyrosine kinase, receptor-related 2).
 GN ROR2 OR NTRK2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Maslakowski P., Carroll R.D.;
 RT "A novel family of cell surface receptors with tyrosine kinase-like
 domain";
 RL J. Biol. Chem. 267:26181-26190(1992).
 RN (2)
 RP SEQUENCE OF 34-943 FROM N.A., AND VARIANT ILE-819.
 RA Oldridge M., Fortuna A.M., Maringe M., Propping P., Mansour S.,
 RA Pollitt C., Dechlara T.M., Kimble R.B., Valenzuela D.M.,
 RA Yancopoulos G.D., Wilkie A.O.M.;
 RT "Dominant mutations in ROR2, encoding an orphan receptor tyrosine
 RT kinase, cause brachydactyly type B";
 RL Nat. Genet. 24:275-278(2000).
 RN (3)
 RP SEQUENCE OF 34-574 FROM N.A., AND VARIANT THR-245.
 RA Schwabe G.C., Tinschert S., Buschow C., Melnick P., Wolff G.,
 RA Gillissen-Kaesbach G., Oldridge M., Wilkie A.O.M., Koemec R.,
 RA Mundlos S.;
 RT "Distinct mutations in the receptor tyrosine kinase gene ROR2 cause
 RT brachydactyly type B";
 RL Am. J. Hum. Genet. 67:822-831(2000).
 RN (4)
 RP VARIANTS RRS C-184; W-189; W-366 AND K-620.
 RA MEDLINE-20392394; PubMed-10932186;
 RA Afzal A.R., Rajab A., Fenske C.D., Oldridge M., Elanko N.,
 RA Terres-Pereira E., Tunesuez B., Murday V.A., Patton M.A.,
 RA Wilkie A.O.M., Jeffery S.;
 RT "Recessive Robinow syndrome, allelic to dominant brachydactyly type B,
 RT is caused by mutation of ROR2";
 RL Nat. Genet. 25:419-422(2000).
 RN (5)
 RP VARIANT RRS TYR-182.
 RA MEDLINE-20392395; PubMed-10932187;
 RA van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,
 RA Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;
 RT "Mutation of the gene encoding the ROR2 tyrosine kinase causes
 RT autosomal recessive Robinow syndrome";
 RL Nat. Genet. 25:423-426(2000).
 RN (6)
 RP ERRATUM.
 RA van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,
 RA Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;
 RL Nat. Genet. 26:383-383(2000).
 CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHICH MAY BE INVOLVED
 CC IN THE EARLY FORMATION OF THE CHONDROCYTES. IT SEEMS TO BE
 CC REQUIRED FOR CARTILAGE AND GROWTH PLATE DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING EARLY
 CC EMBRYONIC DEVELOPMENT. THE EXPRESSION LEVELS DROP STRONGLY AROUND
 CC DAY 16 AND THERE ARE ONLY VERY LOW LEVELS IN ADULT TISSUES.
 CC -1- DISEASE: DEFECTS IN ROR2 ARE A CAUSE OF BRACHYDACTYL TYPE B
 CC (BDB). BDB IS AN AUTOSOMAL DOMINANT SKELETAL DISORDER
 CC CHARACTERIZED BY HYPOPLASIA/APLASIA OF DISTAL PHALANGES AND NAILS.
 CC IN BDB THE MIDDLE PHALANGES ARE SHORT BUT IN ADDITION THE TERMINAL
 CC PHALANGES ARE RUDIMENTARY OR ABSENT. BOTH FINGERS AND TOES ARE

CC AFFECTED. THE THUMBS AND BIG TOES ARE USUALLY DEFORMED.
 CC -1- DISEASE: DEFECTS IN ROR2 ARE A CAUSE OF RECESSIVE ROBINOW SYNDROME
 CC (RRS). RRS IS AN AUTOSOMAL DISORDER CHARACTERIZED BY SKELETAL
 CC DYSPLASIA WITH GENERALIZED LIMB BONE SHORTENING, SEGMENTAL DEFECTS
 CC OF THE SPINE, BRACHYDACTYL AND A DYSMORPHIC FACIAL APPEARANCE.
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE ROR SUBFAMILY.
 CC -----
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 CC EMBL: AF280300; AAG3132.1; JOINED.
 CC EMBL: AF280301; AAG3132.1; JOINED.
 CC EMBL: AF280302; AAG3132.1; JOINED.
 CC EMBL: AF280303; AAG3132.1; JOINED.
 CC EMBL: AF280304; A

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FT DOMAIN 473 746 PROTEIN KINASE.
FT DOMAIN 753 782 SER/THR-RICH.
FT DOMAIN 784 857 PRO-RICH.
FT DOMAIN 859 882 SER/THR-RICH.
FT NE_BIND 479 487 ATP (BY SIMILARITY).
FT BINDING 507 507 ATP (BY SIMILARITY).
FT ACT_SITE 615 615 BY SIMILARITY.
FT MOD_RES 646 646 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT DISULFID 83 135 BY SIMILARITY.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 182 182 C -> Y (IN RRS).
FT VARIANT 184 184 /FTID-VAR_010911.
FT VARIANT 189 189 R -> C (IN RRS).
FT VARIANT 189 189 /FTID-VAR_010768.
FT VARIANT 245 245 R -> W (IN RRS).
FT VARIANT 245 245 /FTID-VAR_010769.
FT VARIANT 366 366 A -> T.
FT VARIANT 366 366 /FTID-VAR_010912.
FT VARIANT 620 620 R -> W (IN RRS).
FT VARIANT 620 620 /FTID-VAR_010770.
FT VARIANT 819 819 N -> K (IN RRS).
FT VARIANT 819 819 /FTID-VAR_010771.
FT SEQUENCE 943 AA; 104726 MW; DBAC1E4622B5ECA0 CRC64;

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Query Match 19.28; Score 876; DB 1; Length 943;
Best Local Similarity 28.68; Pred. No. 4.9e-51;
Matches 236; Conservative 119; Mismatches 249; Indels 222; Gaps 26;

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QY 126 PPIVKKIIEGKAVLPCTMGNPSPVSMIGKDSPLRENSRIAVL---ESGS-LRIHNWQ 181
DB 67 PVNNITIVQGFALHCKVAGNPPNPNWMLNDAPVYQEPRIIRIKREYSRLRIQDLD 126
QY 182 KEDAGQRCVAKNSLGTAKVVKLEFEVFAILRAPESHNVTFGSFVTLHCTATGIPVP 241
DB 127 TTDGYGVQCVATNGMKT-----ITATGV--- 149
QY 242 TITMIENNNVSSGSIQSVKDRVIDSLQLEFTRKPGIYTCIATNKKHGEKSTKAATI 301
DB 150 -----LKV----- 158
QY 302 SIAMSKPKQDNKGCAQYRGEVNCNAVLAQDALVFLNTSYADPREAQ---ELVHTAMNE 358
DB 159 SPNNHFODDYHEDGFCQYRGICACARFIGN-----RTIYVDSLQMGCEINRITAAFTM 212
QY 359 LKV---VSPVCRPAAEALCNHIFQEC-SPGVVPRPIPTICREYCLAVKELCAKEMLYME 414
DB 213 IGTSHLSDDQSOFAIPSCFHFVPLCDARSAPRPRELDCDECEVLESLDCEKYTA- 271
QY 415 EKHTRGLVRSF---MHLISVPCSKLPSMMDPTA---CARLP-----HLDVN--- 456
DB 272 -----KSNPLILMIQLDLPKCALP- MPESPDAANCMRIGITAEKRLGRTHOCYNSGM 322
QY 457 -----KKNLKTFF-----PMTSKSPVDIPNL----- 478
DB 323 DYRGTAFTTKSGHQQPVALQHPHSNHSSTDPDELGGHAUCYRNPQMGEGMFCFTQNK 382
QY 479 -----PSSSSSFVSFPTYSMTVITISMSFAT-FULLITTTLYC-CRRKKOMYK 527
DB 383 NVRMELCDVPSCSPRDS-----KMGILYILVPSIAIPVLVACLCEFLVCMGR-----NK 431
QY 528 KRESAAV---TLTIPSELLDRNRPMTQORMLPLNPLLSL-EYPRNNIEYVRDIG 582
DB 432 QKASASTPQRQLMASPSQDM-----EMPLINOHQAKIKELISLSAVRMEELG 480
QY 583 EGAGGVFOARAPGLLPYPTTNAVKMLKEASADQADQREVALAAEFDPNPIVLL 642
DB 481 EDRGKVVKGLLPGRAPRGEOQVAVALIKTLKKAESRLREERHNEMLMARQHPNVVCLL 540

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QY 643 GVCAGVPRMCLLFEPYMAVDLINEFLRSNPHTVCSLSHSLDSMRAOYSSPGPPPLSCAQ 702
DB 541 GVVTKDPLMSIFSYCSHGDLHEFLVMSRPSHSDVGSTDDDTVSALAEPP-----DF 592
QY 703 LCIRQVAAAGNATYSEKRFVTRDLATRCVLGENMMYKIADEGLSRNITSDYKANKEND 762
DB 593 VHLVAQIAAGEVYLSHHVARKDLATRVLYDKLANKISDGLFEVRYADYKLLGNS 652
QY 763 AIPTRMPPEISIFPNRYTTESDVMAGVVLMEIFSYGLQPYGMAHEVYIYVRDGNILS 822
DB 653 LIPTRMAPEAIKNGKSIDSDISYGVLMVEVSYGLQPYCGSYNDYVMIINRQVLP 712
QY 823 CPENCPELVYLMRLCWSKLPAADPSTSHRILERMCAEAGTGS 868
DB 713 CPDCCPAWVYALMIECWNEFPSRRPRFKDHSRL-----RAMGNLS 753

RESULT 5
TRKB_MOUSE STANDARD; PRT; 821 AA.
AC P15209;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BDNF/NT-3 growth factors receptor precursor (BC 2.7.1.112) (TrkB
DE tyrosine kinase) (GPI45-TrkB/GP95-TrkB) (Trk-B).
GN NTRK2 OR TRKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (GP145).
RC TISSUE=Brain;
RX MEDLINE=90059970; PubMed=2555172;
RA Klein R., Parada L.F., Coulier F., Barbacid M.;
RT "trkb, a novel tyrosine protein kinase receptor expressed during
RL mouse neural development."
RL EMBO J. 8:3701-3709(1989).
RN [2]
RP SEQUENCE FROM N.A. (GP95/Tr1).
RC TISSUE=Brain;
RX MEDLINE=90263089; PubMed=2160854;
RA Klein R., Conway D., Parada L.F., Barbacid M.;
RT "The trkb tyrosine protein kinase gene codes for a second neurogenic
RL receptor that lacks the catalytic kinase domain."
RL Cell 61:647-656(1990).
RN [3]
RP FUNCTION.
RX MEDLINE=91249395; PubMed=1645620;
RA Soppet D., Escandon E., Maragos J., Middlemas D.S., Reid S.W.,
RA Blair J., Burton L.E., Stanton B.R., Kaplan D.R., Hunter T.,
RA Nicolics K., Parada L.F.;
RT "The neurotrophic factors brain-derived neurotrophic factor and
RT neurotrophin-3 are ligands for the trkb tyrosine kinase receptor ";
RL Cell 65:695-903(1991).
CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC GAMMA-1.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST THREE FORMS ARE PRODUCED BY
CC ALTERNATIVE SPLICING; THESE ARE: GPI45-TRKB, T1 (GP95-TRKB) AND
CC T2.
CC -1- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY
CC EXPRESSED IN VARIOUS CELL TYPES. THE T2 ISOFORM IS PRIMARILY
CC EXPRESSED IN NEURONS.

```

CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M33385; AAA0482.1; -
DR EMBL: X17647; CAA35636.1; -
DR PIR: S06943; S06943.
DR PIR: A35104; A35104.
DR HSSP: P1362; 1FGK.
DR MGD: MGI:97384; NTRK2.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR002011; Receptor_Tyr_Kin_II.
DR Pfam: PF00047; 1g; 1.
DR Pfam: PF00560; LRR; 1.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01462; LRRNT; 1.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00082; LRCT; 1.
DR SMART: SM00013; LRNT; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
KW Transferrase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW Leucine-rich repeat; Repeat; Immunoglobulin domain;
KW Alternative splicing.
FT SIGNAL 1 31
FT CHAIN 32 821
FT DOMAIN 32 429
FT TRANSMEM 430 453
FT DOMAIN 454 821
FT REPEAT 72 93
FT REPEAT 96 117
FT DOMAIN 214 270
FT DOMAIN 301 365
FT DOMAIN 537 806
FT NP_BIND 543 551
FT BINDING 571 571
FT ACT_SITE 675 675
FT MOD_RES 515 515
FT MOD_RES 701 701
FT MOD_RES 705 705
FT MOD_RES 706 706
FT MOD_RES 816 816
FT SITE 515 515
FT SITE 816 816
FT CARBOHYD 67 67
FT CARBOHYD 95 95
FT CARBOHYD 121 121
FT CARBOHYD 178 178
FT CARBOHYD 205 205

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 466 476 PASVSNDDDS -> FVLEHKLPLDGG (IN ISOFORM GP95-TRKB/T1).
FT VARSPIC 477 821 MISSING (IN ISOFORM GP95-TRKB/T1).
SQ SEQUENCE 821 AA; 92133 MW; 50E08D5FF68D8F30 CRC64;

Query Match 18.9%; Score 862; DB 1; Length 821;
Best Local Similarity 28.5%; Pred. No. 3; Se 50;
Matches 259; Conservative 121; Mismatches 254; Indels 276; Gaps 34;

QY 34 LETVDALVEEVAFTMCVAVSEYPOPEISWTRNKILIKLFTDRYSIRE-----NGO 82
DB 96 LFTVDSGLKFEVA-YKAFKLNNSNLRHINFTIRNKL-----TSLRRFRHLDLSDLLTGN 148
QY 83 -----LTIILVEDSD--GIYCTANN--VGAVESGALQVKKPKITRP 126
DB 149 PFTSCDLMKLTLOFTKSSPTODLYCLNSESKNPLANTLOIPNCGL-----PSARLA 202
QY 127 PIVNKIIEGLKAVLPCTTGNPKPSVSWIKGD---SPLRENSIANLVESGSLRIHNVQKE 103
DB 203 ARLNLYVEEKSVTLSGSGVDPLTYVDVGNLVSKHNMETSH---TGSRLRTNISSD 258
QY 184 DAG-QYRCVAKNSLGTAVSKV-VKLEFEVFAIRLRAPEASHN---VTFGSFVTLHCATGTI 238
DB 259 DSGKQISCAVENLVGEDDSVNLTVHFAPTITFLESPTSDDHMCIP-----TYRGN 310
QY 239 RVPITTIENGNAVSSGSITQESVKDRVIDSR-----LQLFITRP-----GLYTCTATNKH 288
DB 311 KPAALQWETNG--ALINESYICTKHVNTHTYHCGCLD--DNPTHMNGDITLVAKKNY 367
QY 289 GEKSTAKAAATISIAEWSKPOKMGYCAOYRGEVCANVLAKDALVFINTSVADPEAO 348
DB 368 G-----KDERQISAHNMG----- 380
QY 349 ELLVHTANNELVSPVCPRAAEALLCHIFQESGPGVPTPTPICREYCLAIVKEFCAR 408
DB 381 -----RPGVD-----YETNP-----NYPEVLVE----- 398
QY 409 EMLVNEEKTHRLGYRSEMHLLSVPCSKLPSMHMPPTACARLPHLDYKNEKTKTPRMTS 468
DB 399 DWT-----PTDIGTT-----NKS----- 414
QY 469 SKPSVDIPLNDSSSSSFVSPTYSMTVIISMSFAIFVLTITTLVCCRKKOMKMK 528
DB 415 ELPSTDVAD--QSNREHLSV--YAVVVIASVVG---FCLLVMLLLKLARHSFGMK 465
QY 529 RESAVALTTLTLPSELLRLRHPNPKY-----RNPILLNKL 565
DB 466 PASV-----ISNDDASAPLHHSNGSNTPSSSEGGDAVIIGMTKIPVENOY 515
QY 566 LSL-----EYPRNNIEVVRDIGEAGFVQARAGLLPYEPFTVAVKMLKE 613
DB 516 FGITNSQLKPTFVOHNIKRNHIVLKRLEGDEGAFVFLAEVCYNLCRBDKTLVAVKTK- 574
QY 614 EASADMDQDFQREALMAEFDPNIVKLLGYCANGKPMCLLFETWAYVDLNEFLRSNPH 673
DB 575 DASDAARDDFREELLNLQHEHVLKYYGVCVEDBPLIMVEFYMKHGDLLKFLRAHPD 634
QY 674 TVCSLSHSDLSMRQVSSGPPP--LSCABDLCIAROVAAMAVLSEKKFVHRDLATPNC 731
DB 635 AV-----LMAEGNPTELTOSOMLHIAQIUAAGVYTLASGHFVRDLATPNC 681
QY 732 LVGENNAVVKIADFGISRNYSADYYKANENDAIPIRMPRPESIFYNRYTTSDDWAYGVV 791
DB 682 LVGENLVKLTIGDFGMSRDVYSTDYRVGGHMLPIRMPRPESIMYRKRTTSDVMSLGVV 741
QY 792 LMEIFSGIQQYGYMAHEEVIYVRDGNILSCPENCPEVLYNLMLRCLSKPLPADRPST 851

[illegible][illegible]

```

FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 467 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT PASVISNDDS -> FVLPHKIPIDG (IN TRUNCATED
FT ISOFORM).
FT VARSPPLIC 478 822 MISSING (IN TRUNCATED ISOFORM).
FT VARIANT 338 338 N -> Y (IN DBSNP:1047856).
FT SEQUENCE 822 AA, 91998 MW, 2FE915948FD013 CRC64;

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Query Match 18.8%; Score 861; DB 1; Length 822;
Best Local Similarity 29.5%; Pred. No. 4,1e-50;
Matches 253; Conservative 115; Mismatches 269; Indels 222; Gaps 30;

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OY 59 ISSTRKILIKLEDTKYSTRENQQL-----TILSEDSDD--GIYCGT 100
DB 120 INTRNK-LTSLSRKHRLDLSELVLGNPFTGCDIMWIKILOBAKSSPDODLYCLN 178
OY 101 ANNG-----VGAVESGALQVKKPKITRPINVKITIEGKAVLPCTTGPNKPSVSWIK 156
DB 179 ESSKNIPLANLOIPNCGL-----PSANLAARPLTYEBEKSITLSCSVAGDPYNNYMDV 232
OY 157 GD---SPLAENSRIVLESGLRIHNVQKEDAG-QYRCYAKNSLGTAYSKV-VKLEFEVF 211
DB 233 GVLNYSKHNKESH---TQGLRITNISDDSGKQISCAVENLYGHDQSVNLTVHFAPJ 288
OY 212 ARILRAPESHN---VTFGSFVTLHGTANGIPVPTIWMINGNAVSGSIQESVKQVIDS 268
DB 289 IFFLESFSDHIMCIPF-----TVKGNPKPALOMETNG-ALLNESYICTKTHVTHN 339
OY 269 R-----LOLEITKP-----GLYTCTATNKG--EKFSKAATISIAEMSKPQ-----K 311
DB 340 TEYHCLOL--DNPTNHNNGDYTLAKNKYGEKDEKQISAHFGWPGIDGAPNPDVYI 397
OY 312 DNKGCAYOYRGECNANAVLAKDALVFLNLSYARPEEQELVITANNELKYSPVCPRAAE 371
DB 398 EDYGTANDIDGDTNR-----SNEPSTVDYDKTGRHLSYAAVYVAVSVG----- 444
OY 372 ALLCNHIFOECSPPGVVPTPIPCREYCLAVKELFCAKEMLVMEKTHRLYSEMHLLSY 431
DB 445 -----FCL-----LVN-----LFLKL 456
OY 432 PKCSKL-----PS--MHNDPTACARPLHLDYKKNKTKTPPMSTSSPSVDIPNLPSSSSS 485
DB 457 ARHSKFGKPKPASVISNDDSDASPLHHSNGS-----NTPSSSEGG 497
OY 466 FVSPTSMTVILISINSEFAIFVLLTITLYCCRRKQKNNKRSAAVTLTLPSELL 545
DB 498 -----PDAVITGMTKP----- 509
OY 546 DRLHNPNYQKMP--LLNPKLISLEYPRNNIEYVNDIGEGAGRFQARAPGLTYEPBT 604
DB 510 --VIENPQYFITSQKLPDFTVQHIKRNHNYLKLREGEAGKVFLECYVNLCEQDKI 567
OY 605 MVAVMYMLKEEASADMOQFOREALMAEFDNPNYKLLGYCAVGRPKMLLEFYAAYGLN 664
DB 568 LVAVYTKL-DASDNARKKPFHEDELITLNLQHEHITKRYGVCESGRLMTVEYKMHGDLN 626
OY 665 EFLNSMSPHTVCSLSHSDLSKRAOYSSPGPPP--LSCAEQLCIAQVANAAYLSERKFV 722
DB 627 KFLRHNGPDV-----LMAEGNPTELTQSOMHINOQAAGVYILASQHFV 673
OY 723 HRDLATRCVLGENNVYKIAFGLSRNIYSADYKANKANDAIPIRMPPESTFYNNRYTE 782
DB 674 HRDLATRCVLGENNLVLTGFGMSRDYVSTDYRVGCHTMLPIRMPPESTIMYRKFTTE 733
OY 783 SDVAYGVVLTWEISYGLQPYGYGMAHEEVIYVRDGNLTSPCKPQVLYLMLRLCWSKL 842
DB 734 SDVMSLGVVLTWEITFYGQPYGYGMAHEEVIYVRDGNLTSPCKPQVLYLMLRLCWSKL 793
OY 843 PADRPSPSTIRILLERKCE 861

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DB 794 PHMRKNKIGITHTLLONLAK 812
RESULT 7
TRKB.CHICK
ID TRKB.CHICK STANDARD: PRT; 818 AA.
AC Q91967; Q91010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TrkB
DE tyrosine kinase) (TrkB-B).
GN TRKB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=95047511; PubMed=7959025;
RA Vinh N., Erdmann K., Heumann R.;
RT "Cloning and sequence analysis of a cDNA encoding a novel truncated
RL form of the chicken TrkB receptor.";
RN Gene 149:383-384(1994).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE=94116452; PubMed=8287802;
RA Dechant G., Biffo S., Okazawa H., Kolbeck R., Potgiesser J.,
RA Barde Y.A.;
RT "Expression and binding characteristics of the BDNF receptor chick
RL trkB.";
RL Development 119:545-558(1993).
CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC GAMMA-1 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: A TRUNCATED NON-CATALYTIC FORM WHICH
CC FUNCTION REMAINS STILL UNCLEAR IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
DR EMBL; X77251; CAAS44468.1; -
DR EMBL; X77252; CAAS44469.1; -
DR EMBL; X74109; CAAS2210.1; -
DR HSSP; P11362; IRTG
DR InterPro; IPR000719; Euk_Dkinase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.

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DR InterPro: IPR002011; Receptor_tyr_kin_II.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00047; 15; 1.
 DR Pfam: PF00560; LRR; 1.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PRO0109; TYRKINASE.
 DR SMART: SM00408; IG2; 1.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00013; LRRNT; 1.
 DR SMART: SM00219; TYRC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR Transferrase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
 KW Phosphorylation; Receptor; Glycoprotein; Neogenesis; Signal;
 KW leucine-rich repeat; Repeat; Alternative splicing;
 KW Immunoglobulin domain;
 FT CHAIN 1
 FT SIGNAL 31
 FT DOMAIN 32 818
 FT TRANSMEM 32 426
 FT DOMAIN 427 450
 FT DOMAIN 451 818
 FT REPEAT 71 92
 FT REPEAT 95 116
 FT DOMAIN 213 269
 FT DOMAIN 300 364
 FT DOMAIN 534 803
 FT NP_BIND 540 548
 FT BINDING 568 568
 FT ACT_SITE 672 672
 FT MOD_RES 512 512
 FT MOD_RES 698 698
 FT MOD_RES 702 702
 FT MOD_RES 703 703
 FT MOD_RES 813 813
 FT SITE 512 512
 FT SITE 813 813
 FT SITE 813 813
 FT CARBOHYD 66 66
 FT CARBOHYD 94 94
 FT CARBOHYD 120 120
 FT CARBOHYD 199 199
 FT CARBOHYD 204 204
 FT CARBOHYD 226 226
 FT CARBOHYD 253 253
 FT CARBOHYD 287 287
 FT CARBOHYD 324 324
 FT CARBOHYD 337 337
 FT CARBOHYD 408 408
 FT VARSPLIC 462 520
 FT VARSPLIC 521 818
 FT SEQUENCE 818 AA; 91736 MW; 152 CRC64;
 Query Match 18.88; Score 858; DB 1; Length 818;
 Best Local Similarity 29.48; Pred. No. 6.5e-50;
 Matches 262; Conservative 118; Mismatches 281; Indels 230; Gaps 35;
 QY 6 NIPVHI-LTIVAFSGTEKLPKAPVITPLTVDALVEVATFMCAVESYPOPEISWTRN 64
 DB 113 NINQIYMSKSKSLKSPFRHGLSLDILVD-----NPKKSC-----ELMKIK- 159
 QY 65 KILKLPFTKRSIRENGGLTILSVESDDGICCTANNVGVGAVSGALQVKK----- 120
 DB 160 -----KFOETK-----YTEADQ-ICYVDNN-----KRIALDMKVPNCDL 195
 QY 121 PKTRPPINVAIIIEGLKAVLCTGTMGNPKPSVSWI-----KGDSPLENSRIAVLES 174

DB 196 PSANLSNNYITVEGKSTLYCOTTCGPPPNVSWVLNLSNHSSTSKN-----PAS 248
 QY 175 LRIHNVQKEDAGQY-KCVAKNSIGTAYSKYVLEFEVFAIRLAPESHVTCSEFT----- 230
 DB 249 LTIKNVSMDSGLMISCVAVENIVEYQVSA---ELTVVF---AP---NITFESTPPH 298
 QY 231 ---LHCTANGIPVPTITWENGNAVSGSIOESVKKRVIDSR-----LQLETKP----- 277
 DB 299 HMCIPFTVKGKPKPTLOMFEFG-AIINSEYICTKIHVINOSYHCLDQ---DNPTHLNN 355
 QY 278 GLYTCTATNKGKFEFTAKAAATISAEWSKPOKDKGYCAQYR---GEVCNAVLAOKDL 334
 DB 356 GAVTLLAKNEYGE-----DEKRDVHMSVPGSGSDIVDPDY 394
 QY 335 VFNTSGADEEAOELLVHTANMLKVSP-VCPAAEALCNHIFQECSPVPPPIPI 393
 DB 395 EYETP-----PND-----LGDITNSNOITSPDVSNKEEDSITYV-----VGIATLV 439
 QY 452 HDYNNKENTKPTPMTSSKPSVDIPNLPSSSSSFSVSPYMTVIISMSFAIVLT 511
 DB 479 HISNGS-----NTPSSSEG----- 493
 QY 512 ITTLCCRRKKKKKRESAAVLTLPSELDDLRLHPNMYORMP-LILNFKLLSLEY 570
 DB 494 -----PDVITGMTKIP-----VIENPOFGITNSQDKFDTFVQHI 529
 QY 571 PRNNEIVRDIGEGAFGRVQARAPGLPYEPPTMAVAKMLKEBASADMOADQREKALM 630
 DB 530 KRHNIVLKEHLEGAFGEFVLAECYNLCPEODKLIVAKTLK-DASDNARKDHRRELL 588
 QY 631 AEPNPVIVLLGCAVCAKGMCLLEFYMAVGDLNEEFLRSMSPHTVCSLSHSDLSMARQVS 690
 DB 589 TNLQHEHIVFYGCVGVDPLIMFEYMKHDLKFLRAIGPDAV-----LMAE 637
 QY 691 SPGPPSCAEOLCIAQVAVAGNAVYLSERKFVHDLATRNCLVGENNVKIADEGLSRNI 750
 DB 638 GNRAELTQSOHMLIAQVIAAGVYLSQHFVHDLATRNCLVGENNLVIGEGMSRDV 697
 QY 751 YSADYYANENDAIPIRMMPESIFRYKRTTESVMAVGVLMFEISGYOPVGMHEE 810
 DB 698 YSTDYVIRGGITMLPIKMPESIMYKRTTESVMSLVGLVLMFEISGYOPVGMHEE 757
 QY 811 VIVYVROGNIISCPENCPELVENIMRLCWSKLPADRPSTSHIRLERMCE 861
 DB 758 VIECITQGRVLRPTCPKEVYDLMGQWQREPMRLINKEIHSLLQNLAK 808
 RESULT 8
 TRKB_RAT STANDARD; PRT; 821 AA.
 ID TRKB_RAT
 AC 063604: 063605: 063606:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE BDNF/NT-3 growth factors receptor precursor (BC 2.7.1.112) (TKB
 DE tyrosine kinase) (GPI45-TKB/GP95-TKB) (TKB-B).
 GN NTKR2 OR TRKB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;
 RX NCBI
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Cerebellum;
 RX MEDLINE=91094826; PubMed=1846020;
 RA Middlemas D.S., Lindberg R.A., Hunter T.;
 RT "tkb, a neutral receptor protein-tyrosine kinase: evidence for a
 full-length and two truncated receptors.";

RL Mol. Cell. Biol. 11:143-153(1991).
 RN [2]
 RP PHOSPHORYLATION SITES.
 RX MEDLINE-94149017; PubMed-8106527;
 RA Middelmas D.S., Meisenhelder J., Hunter T.;
 RT "Identification of TrkB autophosphorylation sites and evidence that
 RT phospholipase C-gamma 1 is a substrate of the TrkB receptor.";
 RT J. Biol. Chem. 269:5458-5466(1994).
 CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
 CC NEUROTROPIN-3 AND NEUROTROPIN-4/5 BUT NOT NERVE GROWTH FACTOR (NGF).
 CC INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
 CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
 CC SUBSTRATES FOR THE TRK RECEPTOR ARE SHC, PI-3 KINASE, AND PLC-
 CC GAMMA-1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS: gp145-TRKB (SHOWN
 CC HERE), t1/gp95-TRKB AND t2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY
 CC EXPRESSED IN VARIOUS CELL TYPES. THE T2 ISOFORM IS PRIMARILY
 CC EXPRESSED IN NEURONS.
 CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -----
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 CC or_send_an_email_to_license@sib-sib.ch](http://www.isb-sib.ch/announce/or_send_an_email_to_license@sib-sib.ch)).
 CC -----
 CC EMBL: M55291; AAA42279.1; -;
 CC EMBL: M55292; AAA42280.1; -;
 CC EMBL: M55293; AAA42281.1; -;
 CC HSSP: P11362; IAGW.
 CC InterPro: IPR000719; Euk_Pkinase.
 CC InterPro: IPR003006; I9_MHC.
 CC InterPro: IPR003598; I9_C2.
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR000483; LRR_Cterm.
 CC InterPro: IPR000372; LRR_Nterm.
 CC InterPro: IPR002011; Receptor_tyr_kin_II.
 CC InterPro: IPR001245; Tyr_Pkinase.
 CC Pfam: PF00047; 1g; 1.
 CC Pfam: PF00560; LRR; 1.
 CC Pfam: PF01463; LRRCT; 1.
 CC Pfam: PF01462; LRRNT; 1.
 CC Pfam: PF00069; Pkinase; 1.
 CC PRINTS: PR00109; TYRKINASE.
 CC SMART: SM00408; IGC2; 1.
 CC SMART: SM00082; LRRCT; 1.
 CC SMART: SM00013; LRRNT; 1.
 CC SMART: SM00219; TYRKT; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;
 CC Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
 CC Leucine-rich repeat; Repeat; Immunoglobulin domain;
 CC Alternative splicing;
 CC SIGNAL 1 31 BY SIMILARITY.
 CC CHAIN 32 821 BDNF/NT-3 GROWTH FACTORS RECEPTOR.
 CC DOMAIN 32 429 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 430 453 POTENTIAL.
 CC DOMAIN 454 821 CYTOPLASMIC (POTENTIAL).

FT REPEAT 72 93 LRR 1.
 FT REPEAT 96 117 LRR 2.
 FT DOMAIN 214 270 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 301 365 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 537 606 PROTEIN KINASE.
 FT NP_BIND 543 551 ATP (BY SIMILARITY).
 FT BINDING 571 571 ATP (BY SIMILARITY).
 FT ACT_SITE 675 675 BY SIMILARITY.
 FT MOD_RES 515 515 PHOSPHORYLATION (AUTO-).
 FT MOD_RES 701 701 PHOSPHORYLATION (AUTO-).
 FT MOD_RES 705 705 PHOSPHORYLATION (AUTO-).
 FT MOD_RES 706 706 PHOSPHORYLATION (AUTO-).
 FT MOD_RES 816 816 PHOSPHORYLATION (AUTO-).
 FT SITE 515 515 INTERACTION WITH SHC PROTEIN (BY
 FT SITE 816 816 SIMILARITY).
 FT SITE 816 816 INTERACTION WITH PLC-GAMMA-1 (BY
 FT SITE 67 67 SIMILARITY).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 466 476 PASVSNDDDS -> FVLFHKRPDGG (IN ISOFORM
 FT VARSPLIC 477 821 MISSING (IN ISOFORM T1).
 FT VARSPLIC 466 474 PASVSNDD -> KGKCAVAFAS (IN ISOFORM T2).
 FT VARSPLIC 475 821 MISSING (IN ISOFORM T2).
 SQ SEQUENCE 821 AA; 92186 MW; 0DDACDA212CDA0E CRC64;
 Query Match 18.7%; Score 854.5; DB 1; Length 821;
 Best Local Similarity 28.3%; Pred. No. 1; le-49;
 Matches 249; Conservative 113; Mismatches 254; Indels 263; Gaps 30;
 QY 59 ISWTRKRIILKLEDFRYSIRE-----NGQ-----LLTILVSDDSD--G 95
 DB 120 INFTRKRL-----TSLSRHRRLDLSLLTGNTFTSCDIMWTKTLQETKSSPDQD 173
 QY 96 IVCCTANN-----VGVAVSCGLQVKKPKITRPINVKIIEGLKAVLPECTMGPKPS 151
 DB 174 LVCLNNSKNTPLANIQINCGI-----PSARLAPNLTVEGSKSVTISCSVGGDPLPT 227
 QY 152 VSMIKGD---SPLENRSKRLAVLESGSLRIHNOKEAG-QYRCVAAKNSLGATASV-VKL 206
 DB 228 LYWDVGNILVSKHNETSH---TQGLRRTINISSDSGQISCAVNAENLVGEDDSVNLTV 283
 QY 207 EEEVFARILRABESH---VTFGSFVTLHCTATGIVPTTIENNAVSSGSIQESVVD 263
 DB 284 HRAPTTFLEPSIDHMKIIP-----YRGNPKPALQWYNG-ALINSEKTYCTAI 334
 QY 264 RVIDSR---LQLTFRK-----GLYTCIATNKGE-----KFSYAKAA 298
 DB 335 HTNHTHYGCIOL--DNPTHMNNGDYTLMAKREYKDEKROISAHFMGRGVGYETNPVY 392
 QY 299 AITISIMSKP-----QDKNGYCAQYRGECVNAVLAKDALVFLANTSYADEEEOQL 351
 DB 393 PEVLVEDWTPPDIGDTKKSNE-----IPSTVADQDTNREHS 431
 QY 352 VHTANMELVSPVPCRAEALLCNHIFQECSPGVVPTPIPCRECSLAVKELFCAKEML 411
 DB 432 VYAVVVIASVVG-----FCLVLM----- 451
 QY 412 VMEKTRGLYSEMHLLSVKOSKL---PS--MHMDPTACARLPHLDYKNENLKTFFP 465
 DB 452 -----LKLARHSKFGMKGPASVSNDDSDASPLRHISNGS----- 487
 QY 466 MTSKSPVDIPNLPSSSSSSFSVSPYISMTVIISMSFAIFVLLITTLTYCCRRKKOMK 525


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Db 613 LDP----- 615
Oy 422 YSEMHLSVPCSKLPS---MHMDPTA--CARLPHLDYKNTKTFPPM--TSSKPSVD 474
Db 616 --SKL-----LPRIGIWPNSLVIYDVTEDSGKYTCIAGNSCKIKREAFLYVYDKPAAB 669
Oy 475 INRLPSSSSSSSVSEPTYSM--TVIISINSSFAIFVLTITLLYCCRRKKOMKKR-ES 531
Db 670 EDEGPPSSHT-----PYKMIOTIGLSVGAAYIITVIGLMFYCKRRKAKRLKKHPBG 722
Oy 532 AAVTLTTLSELLDRHLHNPVQRMPLLNPKLLS-----LTPRNINIEYVD 580
Db 723 EEPHEMCLNGTLLONGOTTAETAEVLTALNIGSSSGASKRSARDKMHFPPNSLQTIYT 782
Oy 581 IEGAGFGRVFOARAPGLPEPFTVAVVLMKEASADQAFORREALMAEFDPNIYK 640
Db 783 LORGEGEVFLAKAGAEDEGALVLYKSL-QTRDEQLQDLFRREAEMFGKLNHNVVR 841
Oy 641 ILGVCAVCKPMLLEFYMAVYGDNLNFRKMSPHYVCSLSHS-DLSKRAOVSSBGPPLSC 699
Db 842 LGLGLREAPPHVAVLEYVDLGLKQFLR-----ISKSKDESLK-----PQPLST 885
Oy 700 ABOLCIAROVAAVMAYLSERKFVHHDLATRNCLVGENVYKTIADGLSRNITYSADYKXAN 759
Db 886 KKKVSLCTQVALGMEHLSNGRFVHNDLARNCLVSAQROVKYSALSKDVINSEYIHR 945
Oy 760 ENDALPIRMWPPESIFFYNRYYTESDVWAVYVLMETFSYGLOPYGMAHEEVIYVYRDGN 819
Db 946 Q-AMIPILRMPEAVLEDFSTKSDVMSFGVLMVEFETGEMPRVPLADEVYLAGKSK 1004
Oy 820 I-LSCPENCPVLLYMLRLCMCKSLPADRPSFSTI 852
Db 1005 TKLPQEGCPRLTKLMORCMAPSPKDRPSFSEL 1038

RESULT 10
TRKC_CHICK
ID TRKC_CHICK STANDARD: PRT: 827 AA.
AC Q91044; Q92022; Q91011;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
kinase) (Trk-C).
CN TRKC.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
OC NCBI_TaxID=9031;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-Embryonic brain;
RX MEDLINE=94338700; PubMed=8060621;
RA Garner A.S., Large T.H.;
RT "Isoforms of the avian TrkC receptor: a novel kinase insertion
disassociates transformation and process outgrowth from survival.";
RL Neuron 13:457-472(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA/FL AND TRKC-3).
RX MEDLINE=93359043; PubMed=8394830;
RA Okazawa H., Kamel M., Kanazawa I.;
RT "Molecular cloning and expression of a novel truncated form of
chicken TrkC.";
RL FEBS Lett. 329:171-177(1993).
RN [3]
RP SEQUENCE OF 378-513 FROM N.A.
RC TISSUE-Embryo;
RX MEDLINE=94084905; PubMed=8261614;
RA Williams R., Backstrom A., Ebendal T., Hallbook F.;
RT "Molecular cloning and cellular localization of TrkC in the chicken
embryo.";
RL Brain Res. Dev. Brain Res. 75:235-252(1993).

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CC CC -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-
CC CC PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS
CC CC ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
CC CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
CC CC tyrosine phosphate.
CC CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -1- ALTERNATIVE PRODUCTS: SEVERAL ISOFORMS ARE PRODUCED BY ALTERNATIVE
CC CC SPLICING GIVING RISE TO RECEPTORS WITH DISTINCT FUNCTIONAL
CC CC CAPABILITIES. THEY DIFFER IN THE EXTRACELLULAR MOTIF (ALPHA OR
CC CC BETA TYPES) AND/OR IN THE KINASE DOMAIN (KI, KD, KT, FL
CC CC RESPECTIVELY FOR INSERTION, DELETION, TRUNCATION AND FULL LENGTH).
CC CC THE SEQUENCE SHOWN HERE IS THAT OF THE ALPHA/FULL LENGTH ISOFORM
CC CC (ALPHA/FL). THE COMBINATIONS ALPHA/FL, ALPHA/KD, AND BETA/KD HAVE
CC CC BEEN FOUND IN BRAIN OF A DAYS 13 AGED EMBRYO. THE KT AND KD
CC CC ISOFORMS FAIL TO STIMULATE TRANSFORMATION, PROCESS OUTGROWTH OR
CC CC SURVIVAL. THE KI ISOFORM EXHIBITS TYROSINE PHOSPHORYLATION IN THE
CC CC ABSENCE OF LIGAND AND IS UNABLE TO MEDIATE SURVIVAL OF NEURONAL
CC CC CELLS.
CC CC -1- DEVELOPMENTAL STAGE: EXPRESSION OCCURS IN THE EMBRYONAL DAY 2 (E2)
CC CC EMBRYO WITH INCREASING LEVELS LATER IN DEVELOPMENT. IN THE E9
CC CC INTERMEDIATE LEVELS ARE FOUND IN BRAIN AND SPINAL CORD WITH
CC CC FOUND IN KIDNEY, LIVER, SKIN AND MUSCLE. LOW LEVELS ARE
CC CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION (BY SIMILARITY).
CC CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC CC PROTEIN KINASES. TRK-TYPE SUPRAMILY.
CC CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC CC -1- CAUTION: THE ADDITIONAL KINASE-DELETED ISOFORM TRKC-3 WHICH
CC CC REPLACES THE KINASE DOMAIN WITH 19 AA INSTEAD OF 39 IN THE KD
CC CC ISOFORM RESULTS FROM A FRAMESHIFT.
CC CC -----
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CC CC -----
CC CC EMBL: S74248; AAB31699.1; -
CC CC EMBL: X59669; CAA42202.1; -
CC CC EMBL: Z30091; CAA82907.1; -
CC CC HSSP: P11362; 1FG1.
CC CC InterPro: IPR0000719; Euk_pkinase.
CC CC InterPro: IPR003599; 1g.
CC CC InterPro: IPR003006; 1g_MHC.
CC CC InterPro: IPR001611; LRR.
CC CC InterPro: IPR000483; LRR_Cterm.
CC CC InterPro: IPR000372; LRR_Nterm.
CC CC InterPro: IPR002011; Receptor_tyr_kin_II.
CC CC InterPro: IPR001245; Tyr_pkinase.
CC CC Pfam: PF00047; 1g. 1.
CC CC Pfam: PF00560; LRR; 2.
CC CC Pfam: PF01463; LRRCT; 1.
CC CC Pfam: PF01462; LRRNT; 1.
CC CC Pfam: PF00069; pkinase; 1.
CC CC PRINTS: PR00109; TYRKINASE.
CC CC SMART: SM00409; 1g; 1.
CC CC SMART: SM00082; LRRCT; 1.
CC CC SMART: SM00013; LRRNT; 1.
CC CC SMART: SM00219; TyRKC; 1.
CC CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
CC CC Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;
CC CC Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
CC CC Leucine-rich repeat; Repeat; Alternative splicing;
CC CC Immunoglobulin domain;
CC CC SIGNAL 1 31 BY SIMILARITY.

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FT CHAIN 32 827 NT-3 GROWTH FACTOR RECEPTOR.
FT DOMAIN 32 430 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 431 455 POTENTIAL.
FT DOMAIN 456 827 CYTOPLASMIC (POTENTIAL).
FT REPEAT 102 125 LRR 1.
FT REPEAT 126 149 LRR 2.
FT DOMAIN 227 288 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 319 382 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 340 382 PROTEIN KINASE.
FT NP_BIND 546 554 ATP (BY SIMILARITY).
FT BINDING 574 574 ATP (BY SIMILARITY).
FT ACT_SITE 681 681 BY SIMILARITY.
FT MOD_RES 518 518 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 707 707 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 711 711 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 712 712 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 822 822 INTERACTION WITH SHC PROTEIN (BY SIMILARITY).
FT SITE 518 518 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
FT SITE 822 822 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 98 MISSING (IN BETA EXTRACELLULAR MOTIF).
FT VARSPLIC 581 619 LAAKRDQRAEELTINQHEHYKFTYVCGDGPLNIF
-> CFEIMLNPISTLPGHSGPLNOGLIVEDVYFSKGRHG
F (IN ISOFORM KD).
FT VARSPLIC 620 827 MISSING (IN ISOFORM KD).
FT VARSPLIC 633 664 AHGPDAMILVDGPRQKAGELGSLQMLHIAQ -> LEDTP
CCLSGAGLRASCTGSSGRVNTSGAGS (IN ISOFORM
KT).
FT VARSPLIC 665 827 MISSING (IN ISOFORM KT).
FT VARSPLIC 713 713 R -> REGPRKQGLSTAWQRHRLAPPAAT (IN
ISOFORM K125).
FT CONFLICT 1 39 MDVSLCTPKCTFWRFELMISIMGDIYLSVACPAKICS
-> MHTCWRIEASDRKLVF (IN REF. 2).
FT CONFLICT 124 124 A -> G (IN REF. 2).
FT CONFLICT 378 378 I -> P (IN REF. 3).
FT CONFLICT 481 496 SPLHINHGILTPSSL -> AHTSTTDTTRFVT (IN
REF. 2).
FT CONFLICT 795 795 W -> C (IN REF. 2).
FT SEQUENCE 827 AA; 93180 MW; AB97373113DCB28A CRC64;
SQ

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Db 245 VADLHSINTHQTNLMTNTHAINLTLVNTSEDNGLFLLCIAENVGMSNAYL-LTVY 303
Qy 211 FARLRAPE-----SHWVGSEVTLHCTATGILPVPTITENGNNV-----SS 254
Db 304 PPRLLTLEEVLEHLEHIAF-----AVH-----GNAPLTHLHNGOVLREPTIIMETYYQ 355
Qy 255 GSTIOESKDVVIDSRLOLFTKTP-----GLYCIATNKHGEKSTAKAAATISIAESKP 309
Db 356 GEVSEGC-----LLENNKPTHYNNNGVITIVATNQLOSANQITIG----- 393
Qy 310 QKDNKGCAQYRGSEVCNAVILAKDALVFLNTSYADPEAQELVHTAMNELKVSPVCRPA 369
Db 394 ----- 393
Qy 370 AEALCNHINQECSPGVPPPIPIREYCLAVKELFCAKEMLVMEKTHRGVREMHLL 429
Db 394 -----HFL 396
Qy 430 SVPKCSKLPSMHMDPTACARLPHLDYKNENLKTPPTSSKPSVDIPNLPSSSSSSPSVS 489
Db 397 EKP-----FPESTDNFVSI-----GDYEVS 416
Qy 490 PTSMIVY-----ISTMSFAIFVLLITITLYCC-----RRKQMKK-----KR 529
Db 417 PTPETITHKPEEDTFGVSIAVGLAFACVLLVFLTMINKYGRKSGFMKGPVAVISGE 476
Qy 530 ESAAVTL-----TTLSELLDLRLHNPMP-----YQRPDLNPLKLSLEY----- 570
Db 477 EDSASPLHINHIGITTPSSL-----DAGPDIVYIGTRPIVENPQYFRQGNCHKPDITYQ 533
Qy 571 --PNNIETVYRDIGEGAFGRVQARAGLLPYEFTVAVAKMLKEASADMDQFOEEA 628
Db 534 HIKRRDVLKRELEGEAFGRVFAECYNLSPTNDKMLVAVAKALDPLA-ARKDFOEAE 592
Qy 629 LMAEFDNPNIYKILGYCAVGMKCLLFEYAYAGDLNFEILMSRPTVCSLSHSDLSRAQ 688
Db 593 LITLQHEHYIKFTGCVGGDDPLINVEIKMKHGLNKLFLAHGPD-----AM 639
Qy 689 VSSGPP-----PLSCAEOLCIAROVAGMAYLSERKFVHRDLATRCNLVGENNVYIAD 743
Db 640 ILVGGPRQAKGELGLSOMLIAQIASGMVYIASQHFVHDLATRCNLVGANLIVIGD 699
Qy 744 FGLSRNITSADYKXANNDALPIRMMPESIFRYRYTESDVMAVGVLMFISYGOPLY 803
Db 700 FGMSRDVYSTDYVVGHTMPLIRWMPPESTIMKRTFTESDVSFGVILMFIPTYGQPW 759
Qy 804 YGMAHEEYIVYVRDGNILSCPEVPELVYLMRLCWSKLPADRPSTSHIRILERM 859
Db 760 FQLSNTEVIEICIGGVLEPRVCPKEVYDMLGCMQREPOQRINIKIYKILHAL 815

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RESULT 11
TRKA_HUMAN
ID TRKA_HUMAN STANDARD; PRT; 796 AA.
AC P04629; P08119; Q9U1U7;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
DE (TRKA transformatory tyrosine kinase protein) (p140-TrkA) (Trk-A).
GN NTRK1 OR TRK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (TRKA-I ISOFORM).
RC TISSUE=Colon.
RX MEDLINE=89181575; PubMed=2927393.
RA Martin-Zanca D., Oskam R., Mitra G., Copeland T.D., Barbacid M.;
RT "Molecular and biochemical characterization of the human trk proto-
oncogene.";
RL Mol. Cell. Biol. 9:24-33(1989).

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RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-95123473; PubMed-7823156;
 RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
 RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
 RT "Human trks: molecular cloning, tissue distribution, and expression
 RL of extracellular domain immunoadhesins.";
 RL J. Neurosci. 15:477-491(1995).
 RP [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97435581; PubMed-9290260;
 RA Indo Y., Mardy S., Tsuruta M., Karim M.A., Matsuda I.;
 RT "Structure and organization of the human TRKA gene encoding a high
 RL affinity receptor for nerve growth factor.";
 RL Jpn. J. Hum. Genet. 42:343-351(1997).
 RP [4]
 RP SEQUENCE OF 399-796 FROM N.A.
 RX MEDLINE-86146854; PubMed-2869410;
 RA Martin-Zanca D., Hughes S.H., Barbacid M.;
 RT "A human oncogene formed by the fusion of truncated tropomyosin and
 RL protein tyrosine kinase sequences.";
 RL Nature 319:743-748(1986).
 RP [5]
 RP SEQUENCE OF 399-796 FROM N.A.
 RX MEDLINE-88196074; PubMed-2966065;
 RA Kozma S.C., Redmond S.M.S., Saurer S.M., Groner B., Hynes N.E.;
 RT "Activation of the receptor kinase domain of the trk oncogene by
 RL recombination with two different cellular sequences.";
 RL EMBO J. 7:147-154(1988).
 RP [6]
 RP FUNCTION.
 RX MEDLINE-91218846; PubMed-1850821;
 RA Hempstead B.L., Martin-Zanca D., Kaplan D.R., Parada L.F., Chao M.V.;
 RT "High-affinity NGF binding requires coexpression of the trk proto-
 RL oncogene and the low-affinity NGF receptor.";
 RL Nature 350:678-683(1991).
 RP [7]
 RP FUNCTION.
 RX MEDLINE-91191557; PubMed-1849459;
 RA Klein R., Jing S., Nanduri V., O'Rourke E., Barbacid M.;
 RT "The trk proto-oncogene encodes a receptor for nerve growth factor.";
 RL Cell 65:185-197(1991).
 RP [8]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE-93315496; PubMed-8325889;
 RA Barker P.A., Lomen-Hoerch C., Genesch E.M., Meakin S.O., Glass D.J.,
 RA Shooter E.M.;
 RT "Tissue-specific alternative splicing generates two isoforms of the
 RL trkA receptor.";
 RL J. Biol. Chem. 268:15150-15157(1993).
 RP [9]
 RP MUTAGENESIS OF TYR-791.
 RX MEDLINE-94179299; PubMed-7510697;
 RA Loeb D.M., Stephens R.M., Copeland T.D., Kaplan D.R., Greene L.A.;
 RT "A trk nerve growth factor (NGF) receptor point mutation affecting
 RL interaction with phospholipase C-gamma 1 abolishes NGF-promoted
 RL peripherin induction but not neurite outgrowth.";
 RL J. Biol. Chem. 269:8901-8910(1994).
 RP [10]
 RP MUTAGENESIS AND PHOSPHORYLATION SITES.
 RX MEDLINE-94206546; PubMed-8155326;
 RA Stephens R.M., Loeb D.M., Copeland T.D., Pawson T., Greene L.A.,
 RA Kaplan D.R.;
 RT "Trk receptors use redundant signal transduction pathways involving
 RL SHC and PLC-gamma 1 to mediate NGF responses.";
 RL Neuron 12:691-705(1994).
 RP [11]
 RP STRUCTURE BY NMR OF 489-500.
 RX MEDLINE-96097066; PubMed-8524391;
 RA Zhou M.M., Ravichandran K.S., Olejniczak E.F., Petros A.M.,
 RA Meadows R.P., Sattler M., Harlan J.E., Wade W.S., Burakoff S.J.,
 RA Fesik S.W.;

RT "Structure and ligand recognition of the phosphotyrosine binding
 RL domain of Shc.";
 RL Nature 378:584-592(1995).
 RP [12]
 RP VARIANT CIPA ARG-577.
 RX MEDLINE-96311294; PubMed-8696348;
 RA Indo Y., Tsuruta M., Hayashida Y., Karim M.A., Ohta K., Kawano T.,
 RA Matsubuchi H., Tonoki H., Awaya Y., Matsuda I.;
 RT "Mutations in the TRKA/NGF receptor gene in patients with congenital
 RL insensitivity to pain with anhidrosis.";
 RL Nat. Genet. 13:485-488(1996).
 RP [13]
 RP VARIANT CIPA PRO-780.
 RX MEDLINE-99192367; PubMed-10090906;
 RA Greco A., Villa R., Tubino B., Romano L., Penso D., Pierotti M.A.;
 RT "A Novel NTRK1 Mutation Associated with Congenital Insensitivity to
 RL Pain with Anhidrosis.";
 RL Am. J. Hum. Genet. 64:1207-1210(1999).
 RP [14]
 RP VARIANTS CIPA P-213; W-649 AND S-714, AND VARIANTS S-85; Y-604 AND
 RP V-613.
 RX MEDLINE-99264238; PubMed-10330344;
 RA Mardy S., Miura Y., Endo F., Matsuda I., Sztriha L., Frossard P.,
 RA Moosa A., Ismail E.A.R., Macaya A., Andria G., Toscano E., Gibson W.,
 RA Graham G.E., Indo Y.;
 RT "Congenital insensitivity to pain with anhidrosis: novel mutations in
 RL the TRKA (NTRK1) gene encoding a high-affinity receptor for nerve
 RL growth factor.";
 RL Am. J. Hum. Genet. 64:1570-1579(1999).
 RP [15]
 RP VARIANTS TYR-604; VAL-613 AND GLN-780.
 RX MEDLINE-99371280; PubMed-10443680;
 RA Glimm O., Greco A., Hoang-Vu C., Dralle H., Pierotti M.A., Eng C.;
 RT "Mutation analysis reveals novel sequence variants in NTRK1 in
 RL sporadic human medullary thyroid carcinoma.";
 RL J. Clin. Endocrinol. Metab. 84:2784-2787(1999).
 RP [16]
 RP VARIANT CIPA VAL-587.
 RX MEDLINE-99250414; PubMed-10233776;
 RA Kotsumoto S., Setoyama M., Hozumi H., Mizoguchi S., Fukumaru S.,
 RA Kobayashi K., Saheki T., Kanzaki T.;
 RT "A novel point mutation affecting the tyrosine kinase domain of the
 RL TRKA gene in a family with congenital insensitivity to pain with
 RL anhidrosis.";
 RL J. Invest. Dermatol. 112:810-814(1999).
 RP [17]
 RP VARIANT CIPA LEU-695, AND VARIANT VAL-613.
 RP TISSUE-Peripheral blood;
 RX MEDLINE-20321341; PubMed-10861667;
 RA Shatzky S., Moses S., Levy J., Plinsk V., Hershkovitz E., Herzog L.,
 RA Shore Z., Luder A., Parvari R.;
 RT "Congenital insensitivity to pain with anhidrosis (CIPA) in
 RL Israeli-Bedouins: genetic heterogeneity, novel mutations in the
 RL TRKA/NGF receptor gene, clinical findings, and results of nerve
 RL conduction studies.";
 RL Am. J. Med. Genet. 92:353-360(2000).
 RP [18]
 RP VARIANTS CIPA PRO-93; ARG-522; ARG-577; CYS-654 AND TYR-674.
 RX MEDLINE-20435070; PubMed-10982191;
 RA Miura Y., Mardy S., Awaya Y., Nihel K., Endo F., Matsuda I., Indo Y.;
 RT "Mutation and polymorphism analysis of the TRKA (NTRK1) gene encoding
 RL a high-affinity receptor for nerve growth factor in congenital
 RL insensitivity to pain with anhidrosis (CIPA) families.";
 RL Hum. Genet. 106:116-124(2000).
 RP [19]
 RP VARIANT CIPA ARG-577.
 RX MEDLINE-20036616; PubMed-10567924;
 RA Greco A., Villa R., Fusetti L., Orlandi R., Pierotti M.A.;
 RT "The gly571arg mutation, associated with the autonomic and sensory
 RL disorder congenital insensitivity to pain with anhidrosis, causes the
 RL inactivation of the NTRK1/nerve growth factor receptor.";
 RL J. Cell. Physiol. 182:127-133(2000).
 CC -I- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH

CC FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-
 CC RECEIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
 CC RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRITICAL
 CC ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION
 CC SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA
 CC SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT
 CC SIGNALING PATHWAY.
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC - SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
 CC - SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; TRKA-I AND TRKA-II (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. BOTH ISOFORMS HAVE
 CC SIMILAR BIOLOGICAL PROPERTIES.
 CC - TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL
 CC CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.
 CC - PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC - DISEASE: THE AMINO END OF SEVERAL DIFFERENT CELLULAR PROTEINS
 CC (SUCH AS NON-MUSCLE TROPOMYOSIN TM30NM) HAS BEEN FOUND FUSED WITH
 CC THE PROTEIN TYROSINE KINASE DOMAIN ENCODED BY NTRK1. THESE SOMATIC
 CC REARRANGEMENT CREATES AN ONCOGENIC PROTEIN.
 CC - DISEASE: DEFECTS IN NTRK1 ARE A CAUSE OF A DISEASE CALLED CIPA;
 CC WHICH IS CHARACTERIZED BY A CONGENITAL INSENSITIVITY TO PAIN,
 CC ANHIDROSIS (ABSENCE OF SWEATING), ABSENCE OF REACTION TO NOXIOUS
 CC STIMULI, SELF-MUTILATING BEHAVIOR, AND MENTAL RETARDATION. THIS
 CC RARE AUTOSOMAL RECESSIVE DISORDER IS ALSO KNOWN AS CONGENITAL
 CC SENSORY NEUROPATHY WITH ANHIDROSIS OR HEREDITARY SENSORY AND
 CC AUTONOMIC NEUROPATHY TYPE IV OR FAMILIAL DYSAUTONOMIA TYPE II.
 CC - SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC - SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC - SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC

Query Match 17.8%; Score 812; DB 1; Length 796;
 Best Local Similarity 26.7%; Pred. No. 7.5e-47;
 Matches 233; Conservative 117; Mismatches 247; Indels 330; Gaps 30;

QY 1 MRELINPIPLHILITLV-----AFSGTEKLPRKAVITITPLEYDALVEEVATPMCA 50
 DB 84 LRLRLGELRLNLTIVSGSLFVAPDAFHPTPLRLNLSPFNLES----- 129
 QY 51 VESYPOEISWTRNKILIKLFTTRYSTIRENGQLTITISVEDSDGICYCTA-----N 102
 DB 130 -----LSW-----KTVGGLSLOELVLSGNDPLSCALRWLQWEE 164
 QY 103 NGVGAVE-----SCGALQVKKRPKITRPINVKITIEGKAVLPCPTM 145
 DB 165 EELGAVPEOKLQCHGCGPLAHMPNASCQVPTLKVOP-----NASVDVGDVLLRCQVE 218
 QY 146 GNEKPSVSWIKGDSPLRENSRIA-VLES-----SLRIHNVQKE-DAGQYRCVAKNSLGT 198
 DB 219 GRLEDAQWV-----LLELDSQATVMKSGGLPSLGLTLAVTSDLNKNKLTCAENGVGR 273
 QY 199 AYKVVVKLEFEVFAIRIIRAPESHNVTFGSFVTLH-----C---TATGIPVFTTWIE 247
 DB 274 A-----EVSVOV-----NVSPFASVOLHTAVEMHMCIPFSVDGQAPASLRLWF 317
 QY 248 NGNAVSSGS-----IOESVKRVYIDSRQLFLITKP-----GLYTCIATATKHKGKFTAK 296
 DB 318 NGSVLNTSTFTFEELPRANETVRHGCRLR--NQPHTVANGNTLLAANFEGQ----- 369
 QY 297 AATITISIAEWSKPODKNGKGYCAQYRGVCNAVLAKDALVFLNTSYADPEEAQELVHTAW 356
 DB 370 ASASIMAAAFNDNPFEEV-----PED----- 389
 QY 357 NELKVVSPVCPRAAEALLCNHIFQESPGVVPPIPICTREYCAVLKELFAKELVWEEK 416
 DB 390 -----PIPV----- 393
 QY 417 THRGLYRSEMHLLSVPRCKSLPSMMDPTGACARLPHLDYKKNKLTFRPMTSSKPSVDIP 476

DB 394 -----SFSPVDNTJSGD-- 406
 QY 477 NLPSSESSSFVSPTSMTVILISMSFAIFVLTITLY-----CCRRKQWNRK---- 527
 DB 407 PVKKEDTPEGV-----SYAVGLAVFACFLSTLLVLYNKKGRNRNFGINRAVL 456
 QY 528 -KRESAAVTL-----TLPSE-----LLIDRLHPNPTORMPLLNPKLISLEYRNN 574
 DB 457 APEDGLAMSLHFMFLGSSSPTEGKSGSLGGHITIEDOYFSDACVHIK-----RD 509
 QY 575 IEVYRDIGEGAFGFPDARAPGLPYEPFVVAAYKMKKEESADMOADFOREALMAEFD 634
 DB 510 IYVKWELGEGAFGFPVFLAECHNLPLPEDOKMLVAYKALK-EASEARQDFOREALLMLQ 568
 QY 635 NPNIYKLLGYCAVAKPKMCLLFYMAYGDLNEFLKMSPHTVCSLSHSDLSRAQVSSPG 694
 DB 569 HQHIVREFGYCTEGRPLLMVEYMRHGDNLNFKLSHG-----DAKLLAGEDVAP 619
 QY 695 PPLSCAQDLTARQVAAAGMAYLSERKRYHNDLATRNCLVGENMYKTADEGLSNISAD 754
 DB 620 GPLGLQLLVAVASQVAAQMYVLADLHFVHDLATRNCLVGGGLVYKIGDEFSMDIYSTD 679
 QY 755 YKKNENDAIPIRMPPESIFNRYTTESDVWAGVYLMFEISYGLOPYGMAHEVYIY 814
 DB 680 YIRYGGRTMLPIRMPPESILYKFTTESDVWSFGVYLMFEITGKQPWYOLSTEAIDC 739
 QY 815 VRDGNILSCPEVCELYNMLCWSKLPADPSFTSIHRIEMCE 861
 DB 740 ITQRELEPRPRACPPEYVALIMRCQCOREPOGRHSIKDVHARLQALQ 786

RESULT 12
 TRKC_HUMAN
 ID TRKC_HUMAN STANDARD; PRT; 839 AA.
 AC Q16288; Q16289; Q12827;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NF-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
 DE kinase) (GPI45-TrkC) (Trk-C).
 GN NTRK3 OR TRKC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=95123473; Pubmed=7823156;
 RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
 RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
 RT "Human trks: molecular cloning, tissue distribution, and expression
 RT of extracellular domain immunoadhesins.";
 RL J. Neurosci. 15:477-491(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=fetal brain;
 RX MEDLINE=95104834; Pubmed=7806211;
 RA McGregor L.M., Baylin S.B., Griffin C.A., Hawkins A.L., Nelkin B.D.;
 RT "Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal
 RT assignment, and evidence for a splice variant.";
 RL Genomics 22:267-272(1994).
 CC - FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-
 CC PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS
 CC ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC - SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC - ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS OF TRKC ARE PRODUCED BY
 CC ALTERNATIVE SPLICING. THE DIFFERENT ISOFORMS DO NOT HAVE IDENTICAL
 CC SIGNALING PROPERTIES. THE ISOFORM B IS EXPRESSED IN A RELATIVELY

CC LARGE AMOUNT IN THE ADULT BRAIN COMPARATIVELY TO FETAL BRAIN.
 CC - TISSUE SPECIFICITY: WIDELY EXPRESSED, MAINLY IN THE NERVOUS
 CC TISSUE.
 CC - P.TM. LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
 CC - SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
 CC - SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
 CC - SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: S76475; AAB3311.1; -
 DR EMBL: S76476; AAB3312.1; -
 DR EMBL: U05012; AAB75374.1; -
 DR HSPD: P13622; IAGW.
 DR MIM: 191316; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00560; LRR; 2.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01462; LRRNT; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00013; LRRNT; 1.
 DR SMART: SM00219; TYRKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transfaser: Tyrosine-protein kinase: Transmembrane; ATP-binding;
 KM Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
 KM Leucine-rich repeat; Repeat; Alternative splicing;
 KM Immunoglobulin domain.
 KT SIGNAL 1 31
 KT CHAIN 32 839
 KT DOMAIN 32 429
 KT TRANSMEM 430 453
 KT DOMAIN 454 839
 KT REPEAT 102 125
 KT REPEAT 126 149
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 KT SITE 834 834
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 KT CARBOHYD 79 79
 KT CARBOHYD 133 133
 KT CARBOHYD 163 163

FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 529 612 MISSING (IN ISOFORM D).
 FT VARSPLIC 613 839 YVOHKRDIYVLRKREGSGKVFVLAECYNLSPTKDKMLV
 FT VARSPLIC 712 725 AVKALDKPTLAKDFQREAEELTNQHEHYKFGVCGDG
 FT CONFLICT 70 70 DP -> WPSFTLNDNGILNKKRDIHVSHTYIEEPVVO
 FT CONFLICT 635 635 SCEVSPRSGHGREIMNLSIPGSKPLNHOIYEDVAVY
 FT CONFLICT 635 635 ESKGRGE (IN ISOFORM B).
 FT CONFLICT 635 635 MISSING (IN ISOFORM B).
 FT CONFLICT 635 635 N -> S (IN REF. 2).
 FT CONFLICT 635 635 D -> N (IN REF. 2).
 SQ SEQUENCE 839 AA; 94455 MW; 86D965A5003B4DD CRC64;

Query Match 17.3%; Score 792.5; DB 1; Length 839;
 Best Local Similarity 25.9%; Pred. No. 1.6e-45;
 Matches 254; Conservative 125; Mismatches 244; Indels 357; Gaps 38;

QY 6 NPLVHI-----LTVAFGSTKLT-----PKAYITTPLEVDALVEE 43
 DB 79 NITSIHENWRSRSLHTANADVMELVYGLKLTIKNSGLRSIQPAFAKNPRLHYRILNLSNR 138
 QY 44 VAFMCVAVESYPOPEISWTNRNKLILKLPDTRYSIKRENGCLLTLSVED----- 91
 DB 139 LTT-----LSW-----QLFOT-LSLR-----LQLEQNFNCSDIRM 171
 QY 92-----SDGTYCCTANNNGCA-----VESCGALQVMAKRTIRPPINVKI 132
 DB 172 QLMQEGEAKLNSQNLXCINAD-----GSQLPFRMINSOCDL-----PEISVSHNLTV 221
 QY 133 IGLKAVLPCTTMGNPKPSVSMI-----KQDSPRENSRIAVLESGSLRIHNQKEAG-Q 187
 DB 222 REGDNAVITCNGSGSLPVDVITVGLQSLNTHQNLNNTVNAHILTLVNTVTSSENGFT 281
 QY 188 YRCVAKNSLG-----TAY--SKVYKLEFEVFAIRLRAPE--SHNYTFGSFVTLHCT 234
 DB 282 LVCIAENNVGMNASVALTVYVPRVVSIDE-----EPRLREHCHIEF-----V 324
 QY 235 ATGIPVPTTVIENGNAVSSGS--QESVKDRYIDSLRLFITKP-----GLYTCTATNK 287
 DB 325 VSGNPPTLHMLHNGQLRESKTIHVEYVQEEISEGCLLF-NKPRHYNNNGVYTLAKNP 383
 QY 288 HGEKSTAKAATTSIAENSKPOKDNKGCAQYRGECNAVALAKDALVFLNNTSYADPEEA 347
 DB 384 LG-----TANQTLN-----GH-----FLKEPF-PEST 404
 QY 348 QELLVHTANNELVKVVSPVCPRAEALLCNHIFQESPGVVPPIPIRGYCLAVALKEFCA 407
 DB 405 DNF1-----LDEVSP----- 415
 QY 408 KEMLVMEKTHRGIVRSEMHLLSVKCSKLPBMHMDPTGACARLPHDYKKNLKTPTPMT 467
 DB 416-----TPPT 420
 QY 468 -SSKPSVDIPNLSSSSSFVSPTYSMTVIISMSFAIFLTLTTLYCCRRKRWKN 526
 DB 421 VTHKRED-----TFGVSAVGLAFACVLLVLFVLMNKGRSKRFGM 464
 QY 527 K-----KRESAAYTL-----TLPSLLLDRLHPNM---YQRMPLLNPKLLSEY 570
 DB 465 KGPVAVITSGEDSASPLHINHIGITPSSL--DAGPDVVVIGMTRIPVIEINPOYFROGH 521
 QY 571-----PRNIIIEVVDIGGAGFGRVQANRGLLPEYPTMVAVKLKEASND 618
 DB 522 NCHKPDYVQHKRDIYVLRKREGSGKVFVLAECYNLSPTKDKMLVAVALKDKPTLA- 580


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OY 619 MOADFOREALMAEFDPNIVKILGVCAGKMCILFEYMAVGLNIEFLRSMSPHTVCSL 678
    : ||||| : : ||| || : : ||||| : ||||| : ||| :
Db 581 ARKFOREAEELTMOHEHIYKFGVCGDGPLLMFEYMHGDLNLFRAHGDD----- 635
OY 679 SHSDLSMRAQVSSPP-----PLSCAEQLCIANOVAAGMAVLSERKVRHDLATRCNV 733
    : : : : : : : : : : : : : : : : : : : : : : :
Db 636 -----AMILVGOFRQAKGELGSLQMLHIASQIASGVYLASQHFHBDLATRCNV 687
OY 734 GENNVKICADGCSRNITYSADYK-----ANEND-----ALPRMWPESIFNRY 779
    : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 688 GANLVKIGDGMGRDVISTDYRLFNPSGNDPCICEVGGHTMLPRKMPESIMTKFE 747
OY 780 TTESDVAAVGVVLEIFSYGLPYGMAHEEVIYVRDGNILSCPENCPVELYMLMLRCW 839
    : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 748 TTESDVMSFGVILWEIFTYGQPMFQSLNTEVICITGGRVLERPRCPKEVYVLMGCV 807
OY 840 SKLPADRPSTSHIRLERM 859
    : : : : : : : : : : : : : : : : : : : : : : :
Db 808 QREPOQRILNKEIKILHAL 827

RESULT 13
TRKC_PIG STANDARD; PRT; 825 AA.
AC P24786;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NT-3 growth factor receptor precursor (BC 2.7.1.112) (TrkC tyrosine
GN NTRK3 OR TRKC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91364178; PubMed=1653651;
RA Lamballe F., Klein R., Barbacid M.;
RT "trkC, a new member of the trk family of tyrosine protein kinases, is
RT a receptor for neurotrophin-3."
RL Cell 66:967-979(1991).
CC -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-
CC PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS
CC ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY IN THE BRAIN, LOW LEVELS IN THE
CC OVARIES.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M80800; AAA31130.1; -.
CC PIR: A40026; A40026.
CC HSSP: P11362; JFGK.
CC InterPro: IPR000719; Euk_Pkinase.
CC InterPro: IPR003599; Ig.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00560; LRR_2.
DR Pfam: PF01463; LRRCT_1.
DR Pfam: PF01462; LRRNT_1.
DR Pfam: PF00069; Pkinase_1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00409; Ig_1.
DR SMART: SM00082; LRRCT_1.
DR SMART: SM00013; LRRNT_1.
DR SMART: SM00219; TYRK_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ADP_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
DR Transferrase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW Leucine-rich repeat; Repeat; Immunoglobulin domain.
FT SIGNAL 1
FT CHAIN 32
FT DOMAIN 32 429
FT TRANSMEM 430 453
FT DOMAIN 454 825
FT REPEAT 102 125
FT REPEAT 126 149
FT DOMAIN 227 288
FT DOMAIN 319 382
FT DOMAIN 538 814
FT NP_BIND 544 552
FT BINDING 572 572
FT ACT_SITE 679 679
FT MOD_RES 516 516
FT MOD_RES 705 705
FT MOD_RES 709 709
FT MOD_RES 710 710
FT MOD_RES 820 820
FT SITE 516 516
FT SITE 820 820
FT SITE 820 820
FT CARBOHYD 68 68
FT CARBOHYD 72 72
FT CARBOHYD 79 79
FT CARBOHYD 133 133
FT CARBOHYD 163 163
FT CARBOHYD 203 203
FT CARBOHYD 218 218
FT CARBOHYD 232 232
FT CARBOHYD 259 259
FT CARBOHYD 267 267
FT CARBOHYD 272 272
FT CARBOHYD 294 294
FT CARBOHYD 375 375
FT CARBOHYD 388 388
SO SEQUENCE 825 AA; 93129 MW; A3C6716B10D28540 CRC64;

Query Match 17.38; Score 788.5; DB 1; Length 825;
Best Local Similarity 24.28; Pred. No. 2.9e-45;
Matches 234; Conservative 132; Mismatches 255; Indels 347; Gaps 27;

OY 6 NIDPLVHT-----LTLVAFSGTEKL-----PKAPVLTTPLETVDAVVEE 43
Db 79 NITSHIENMRGLHTLVANVDMLTGTGLKLTIKNSGLRSIOPRAFPKPHRYINLSNR 138
OY 44 VATEMCVAVESYPOPEISWTRNKKILIKLFDTRYISIRENGQLTLTISVED----- 91
Db 139 LTT-----LSM-----QLFQT-LSLRE-----LRLBQNFNCSDIRMM 171

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OY 92 -----SDGIIYCCSTANNGVGA-----VESOGALQVYKMKRPTPIINVKI 132
DB 172 QLMQEGEAKLNQSLYICISAD-----GSOLPLFRMNIISQCDL-----PEISHSNLTUV 221
OY 133 IEGKAVNLFCTTMGNPKPVSMTI-----KQDSPRENSRIAVLESGLRIHNQKEDAG-Q 187
DB 222 REGDNVAVVNCNCGSPPLPVDMIVTGLQSIINTHOTNLNNTNVAIMLTIVNTSEONGFT 281
OY 188 YRCVAKNSIGTAYSKV-VKLEFEVFARILRAPE---SHNVTEGSEFVTLCTATGIVPPI 243
DB 282 LUCIAENVGMSNASALVHYHPPRVSLSEEPRLREHCTER-----VVRGNPPPTL 333
OY 244 TWIENGNVSSGSIQESVADYIDSRLOLFTKPLGYTCIATNKHGEKSTAKAATISI 303
DB 334 HMLHNG----- 339
OY 304 AEMSKQKQNKKGCAQREVCNAVLAADALVPLNTSYADPREAQDLVHTANELKAVS 363
DB 340 ---OPLRSK-----ITHVEYQGEVS 359
OY 364 RVCRAPAEALLCNHIFQECSPGVVPTPIRCREYCLAVKELFCAKEMLVMEETKTRGLYR 423
DB 360 ECG-----LLENKPTH----- 370
OY 424 SEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEN--LKTERRMTSSKPSVD----- 474
DB 371 -----YNGNYTLNROPELPTANOTINGHFLKRP 399
OY 475 IPNLPSSSSSFSVSPTSMTVI-----ISIMSFALIVLITLTYCCRRKKQK 525
DB 400 PESTDNEVSYFEVPTPTITVTHKREEDTPGVSTAVGLAFAVCYLVLFIMINKYGR 459
OY 526 NKRRESAATLTTLPSSELLDLRLHPMYO-----RMPLLNPKLSTL 568
DB 460 SFKGMKGAVALVSGEEDSAPLHNDOPMHHNHTLIGRAGHSVIGMTRIPVLENPOYFQ 519
OY 569 EY-----PRNNIEYVRDIOEGAFGRVFOARAGDGLLYPERFTVAVAKMLEAS 616
DB 520 GNCHHKPDTYVOHIKRRDYLKRELEGEAFGVFLAECYNLSPTKYKMLVAVKALDPTL 579
OY 617 ADMQADFOREALMAEFDPNITVILKLGCAVCKPMCLFREYAAVYDGLNEFLRSMSPHTVC 676
DB 580 A-ARQDFQAEALTLNLOHEHIVKFTYGVCGDDPLTWFEIKHGDNLKLRHNGD--- 635
OY 677 SLHSDLSMRAQVSSPCPP-----PLSCAEOLCIARQVAGNAVYLSERKFEVHDLATRNC 731
DB 636 -----AMILVDCGRQAKGELGSLQMLHIASQISGVYLASQHFVHRDLATRNC 685
OY 732 LVGENNVVAILADFGLSRNIYSADYKXANENDAIPIKMPPESEIFYKRTTESDYNAVYV 791
DB 686 LVGANLTVIKIGFGMSRDYSTDYRVVGGHTMLPIKMPPESEIMYKRFTESEVMSFGYI 745
OY 792 LMEIFSGLQPYGYMAHEEVIYVVRGNTLSCPENCPVLVYNNMLRCLMWSKLPADRSPTS 851
DB 746 LMEIFLYGQPMFQSLNTEVIECTIOGRVLERPRVCPRKEVYIDVMLGCMQREPORLIKE 805
OY 852 IHRILERM 859
DB 806 IYKILHAL 813

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RESULT 14
TRKA_RAT
ID TRKA_RAT STANDARD: PRT: 799 AA.
AC P35739:
DT 01-JUN-1994 (Rel. 29, Last Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
DE (p140-TrkA) (Slow nerve growth factor receptor) (Trk-A).
GN NTRK1 OR TRKA OR TRK.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (TRKA-II ISOFORM).
RX MEDLINE=92196121; PubMed=1312719;
RT "Meakin S.O., Suter U., Drinkwater C.C., Welcher A.A., Shooter E.M.;
RT "The rat trk protooncogene product exhibits properties characteristic
RT of the slow nerve growth factor receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2374-2378(1992).
RN [2]
RP ALTERNATIVE SPLICING.
RX MEDLINE=93315496; PubMed=8325889;
RA Barker P.A., Lomen-Hoerth C., Gensch E.M., Meakin S.O., Glass D.J.,
RA Shooter E.M.;
RT "Tissue-specific alternative splicing generates two isoforms of the
RT trkA receptor.";
RL J. Biol. Chem. 268:15150-15157(1993).
CC -1- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH
CC FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-
CC DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
CC RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRUCIAL
CC ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION
CC SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA
CC SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT
CC SIGNALING PATHWAY (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; TRKA-I AND TRKA-II (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. BOTH ISOFORMS HAVE
CC SIMILAR BIOLOGICAL PROPERTIES.
CC -1- TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL
CC CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC or send an email to license@sib.ch).
CC -----
DR EMBL: M85214; AAA42286.1; -
DR EMBL: L12225; -; NOT_ANNOTATED_CDS.
DR PIR: A41981; TVRTTB.
DR HSPD: P11362; IFCG.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00560; LRR_2.
DR Pfam: PF00069; pkinase_1.
DR PRINTS: SM00109; TYRKINASE.
DR SMART: SM00409; IG_1.
DR SMART: SM00082; LRRCD_1.
DR SMART: SM00219; TYRK_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
DR Transferase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Leucine-rich repeat; Immunoglobulin domain; Neurogenesis;

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DR EMBL: U3635; AAA87565.1; -
 DR EMBL: U40271; AAC50484.1; -
 DR HSSP: P12931; 1FMK.
 DR MIM: 601890; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003588; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Ig; 7.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00410; IG_Like; 2.
 DR SMART: SM00408; IGC2; 5.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 30
 FT CHAIN 1 1070
 FT DOMAIN 31 1070
 FT TRANSMEM 31 704
 FT DOMAIN 705 725
 FT DOMAIN 726 1070
 FT DOMAIN 46 108
 FT DOMAIN 143 208
 FT DOMAIN 239 308
 FT DOMAIN 336 398
 FT DOMAIN 426 488
 FT DOMAIN 517 577
 FT DOMAIN 606 671
 FT DOMAIN 796 1066
 FT DISULFID 53 101
 FT DISULFID 150 200
 FT DISULFID 246 301
 FT DISULFID 343 391
 FT DISULFID 433 481
 FT DISULFID 524 570
 FT DISULFID 613 664
 FT CARBOHYD 116 116
 FT CARBOHYD 175 175
 FT CARBOHYD 184 184
 FT CARBOHYD 214 214
 FT CARBOHYD 268 268
 FT CARBOHYD 283 283
 FT CARBOHYD 405 405
 FT CARBOHYD 463 463
 FT CARBOHYD 567 567
 FT CARBOHYD 646 646
 FT CONFLICT 92 92
 FT CONFLICT 147 147
 FT CONFLICT 207 207
 FT CONFLICT 495 496
 FT CONFLICT 515 515
 FT CONFLICT 834 834
 FT CONFLICT 881 881
 FT CONFLICT 969 969
 FT CONFLICT 992 992
 SO SEQUENCE 1070 AA: 118260 MW: 47025386369845 CRC64;

Query Match 16.9%; Score 774; DB 1; Length 1070;
 Best Local Similarity 27.2%; Pred. No. 3.9e-44;
 Matches 228; Conservative 137; Mismatches 304; Indels 168; Gaps 29;

OY 55 POPETSWTRKILIKLFDTRKSTIRENQALLTISVEDSGICYCTANNVGVGAVESGCA 114

Db 350 PERSVMEHAGVRL---PHGRVYQKGHELVLANIAESDAGVYTCNANLAGORODVN- 405
 OY 115 LQYKMKPKITRPINVKIIEGLKAVLPCTTGNPKPSVSIKGDSPLENSRIAVLESQS 174
 Db 406 IYVATVPMSLKKRQDSQLEBGRGYDLCULQATPKFTVWYRQMLISEDSREYVKNST 465
 OY 175 LRTHNQKEDAGQRCVANKSLGTAISKVYKLEFEVFAIRLAP---ESHNTFGSFVTL 231
 Db 466 LRINSVEYDGTWYRCMSTSPAGSIEAQAV---LQVLEKIKFPPQPOOCMGDFKEAV 522
 OY 232 HCTATGIPVPTITWINGNANVSGSIOESVKDRVIDSRQLQFLTK-----PGLYCTIAN 286
 Db 523 PCSATGREKPTIKMER-----ADGS---SLPEVYDINAQTLHFAVTRRDAGNYCTIASN 574
 OY 287 KKGKFKSTAKAATATSIASWSPQKDKNGYCAQYRGECNAVLKDALVFLNTSYADPEE 346
 Db 575 -----GPOQGIKRAHVQLVY-----ANFI--TFKPEPR 600
 OY 347 AQELLVHTAMNELKVSPVCRPAEALLCNHIFQESPGVVPPIPICRHYCLAVKEIFC 406
 Db 601 TTVYQGHIA-----LLOCEAOGDKPL----- 622
 OY 407 AKEMLVMEKTRHGLYRSEMHLISVPKCSKLPSM-----WDPTACARLPILDY 455
 Db 623 -IQW-----KQDRILDPKLG--PRMHIFQGSIVINDVAPEDSGRTTCIAG 667
 OY 456 NKENLK-TFPPMTSSKPSYDINLPSSSSSSFSVSPYSM--TVIISWSPFAIVLTI 512
 Db 668 NSCNKHKHEAPLY---VYDKP-VPESESGPS-PPYKMIQTIGLSVGAATAVAVLG 721
 OY 513 TLYC---CRRKQKNNKRRSAVTL-----TTLPSELLDLRHPNMQRM 557
 Db 722 LMFYKRRKKAKARLOKQEBGEPEMECLNGRPLONGQPSAEIOEBVALTSGSGPAATNK 781
 OY 558 PLLNPKLISLEYRNNIYEVYRDIGEGAFGRVFOARGLPYEPFTWAVAKLKEEASA 617
 Db 782 RHSTSDK---MHFPSSLIQPTITLTKSEFGEVFLAKAGLEGVAETLVVKSLSQK-DE 837
 OY 618 DMQADFOREALMFEQNPNTIVKLLGVCAGVKPKCLLEFYNAVYGDLEFLMSMSPHYCS 677
 Db 838 QOQDLFRRELEFGKLNANAVRRLGLCREAPHYMVEYVDLEDKQFLR----- 888
 OY 678 LSHS-DLSMRAQVSSPPPLSCAEQLCIARQVAAQMAVLSERKPHVDLATRNCLVNS 736
 Db 889 ISKSKDEKLKQO-----PLSTQKVALCTQVALGHEHLSNNRPHVDLARNCLVSAQ 941
 OY 737 MVYKIDPGLSRLNIYSADYKANENDALPIKMPDESIYRNRYTTESDVMAVGVLMET 796
 Db 942 ROVAVSALGSKDYVNSEYHFRQ-AWVALRWMSPEALLEGDFSTKSDVMAVGLVMEVF 1000
 OY 797 SYGLQPYVGMHEVITYYVRDGNL-LSCPEMCPVEIVNLMCLSKSLPADRPSTSI 852
 Db 1001 THGEMPHQGDVDEVLADLGAKRLPQPEGCSKLYRLMQRWALSPKDRPSPSEI 1057

Search completed: August 16, 2002, 13:37:06
 Job time: 66 sec

CC method uses a mutated PKR nucleic acid which comprises a modification
to the intracellular and extracellular domains, or comprises a
modification to the intracellular domain and excludes any nerve growth
CC factor receptor(s) (NGFR). The method uses mutated PKR as a cell
CC surface marker, and is useful for identifying genetically modified cells,
CC especially immunoselection of transduced mammalian cells, and for
CC identifying mammalian cells expressing a protein of interest. The
CC genetically modified marked cells may be used in an autologous or
CC allogeneic setting e.g. gene therapy for bone marrow transplants, graft
CC facilitation or immune reconstitution.

50 Sequence 869 AA:

Query Match 100.0%; Score 4569; DB 22; Length 869;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRELNIPIVHLITLVAFSGTEKLPKAPVITPTPLETVDAIVEEATFMCAVESYPOPEIS 60
1 mrelniplvhlitlvafsgteklpkapvittptpletvdaiveeatfmcavesypopeis 60
61 WTRNKILIKLFDRIYSIRENGQLITLISVEDSDGIYCTANNGVGAVESGALGVKMK 120
61 wtrnkililiklfdriysirengqlitlisedsdgiyctannvgavescgalgvkmk 120
121 PRTTRPPIWKIIEGLKVLPCPTMGNPKPSYMWIKGSDPLRENSRIAVLESGLRIHNV 180
121 prttrppiwkiieglkvlpcptmgnpkpsymwikgdsplrensrivalesglrihmv 180
181 OKEDAGQYRCVAKNSIGTAYSVVKEFEVFAIRAPESHNVTEGSEFVTLCHTATGIPV 240
181 okedagqyrcvaknsgtaysvvkefevfarilrapeshnvtegesefvtlchtatgipv 240
241 PRTTWENGNAVSSGSIOSVCKDRITDSRLQFIRKPGIYTCIATNKHEKSTAKAAT 300
241 prttwengnavssgsiosvckdrirtsrlqfirkpigiyciatnkhekstakaaat 300
301 ISIAEMSKPDKNKCQYRGEVCNANAKDALVFLNTSYADPEAOELVHTAMNELK 360
301 isiaemskpdknkcyqrgvecnanaakdalvflntsyadpeaoelvhtamnelk 360
361 VVSPICRAAEALCNHIFOECSPEVPPPIYICREYCLAVELFCAKEMLVMEETKRG 420
361 vvspicraaealcnhifoe cpspevpppiyicreyclavelfcakemlvmeetkrg 420
421 LYRSEMHLSYPKCKLSMHMDPACARLPLDINKENLTKFPMTSSKPSVDIPNTPS 480
421 lyrsemhlisypkcklsmhmdpacarlpldynkenltkfpmstsskpsvdipnps 480
481 SSSSFSVSPYTSMTVIISINSSFAIFVLITTLTYCCRRKQMKKRESAAVLTLP 540
481 ssssfsvspytstvtiisinsfai fvlitlttyccrrkqmkkresaaavltp 540
541 SELLDLRHPMPQRMPLLNPKLSLEYPRNNIERYVDIGEGAFGVQARAPGLPY 600
541 sellldlrhmpmqrmpllnpklsleyprnnieryvdigegafgvqarapglpy 600
601 EPTTAVAVKMLKEBASADMDQDFORALMAEPDNPVTKLVGNCKKPKCLFEVAY 660
601 epttavavkmlkebasadmdqdforalm aepdnptvtklvgnckkpkclfevay 660
661 GDLNEFLRSMSPATVCSLSHSDLSMRAOVSSPPPLSCAQLCIARVAAGMAYLSRK 720
661 gdlneflrsm spatvcs lshsdls mraovssppplsc aqlciarvaagmaylsrk 720
721 FVHEDLFRKLVGENNVAIKADGLSRNITSADYKANENDAIPIRMPPESIFXNRYT 780
721 fvhedlfrklvgennvai kadglsrnits adykanendaipirmppesifxnryt 780
781 TESDVAAYGVVLAIEFSXGLOPYGMAHEEIVYVRDGNITSCBENPVELYNMLCWS 840
781 tesdvaaygvvlaief sxglopygmahee ivyvr dgnitsc benpvelynmlcws 840
841 TEEDVAYGVVLAIEFSYGLPYGMAHEEIVYVRDGNITSCBENPVELYNMLCWS 840
841 teedvaygvvlaief syglpygmahee ivyvr dgnitsc benpvelynmlcws 840

DB 841 KIPADPSTSHRIIRNCEPAGTVSV 869
841 kipadpstshriirncep agtvs 869

RESULT 3
ID AAM26611 standard; Protein; 869 AA.
AAM26611;
27-JAN-1998 (first entry)

Human muscle-specific kinase (Musk).
Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; human.
ligand; agrin; diagnosis; therapy.

Hom sapiens.
(M09721811-A2.

19-JUN-1997.

13-DEC-1996; 96MO-US20696.

10-MAY-1996; 96US-0644271.

15-DEC-1995; 95US-0008657.

(REG-) REGENERON PHARM INC.

Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;

WPI, 1997-332783/30.

DR N-PSDB; AAT90473.

Nucleotide sequences encoding human agrin and muscle specific kinase
and related receptor - used in diagnosis and treatment of disorder
with muscle atrophy

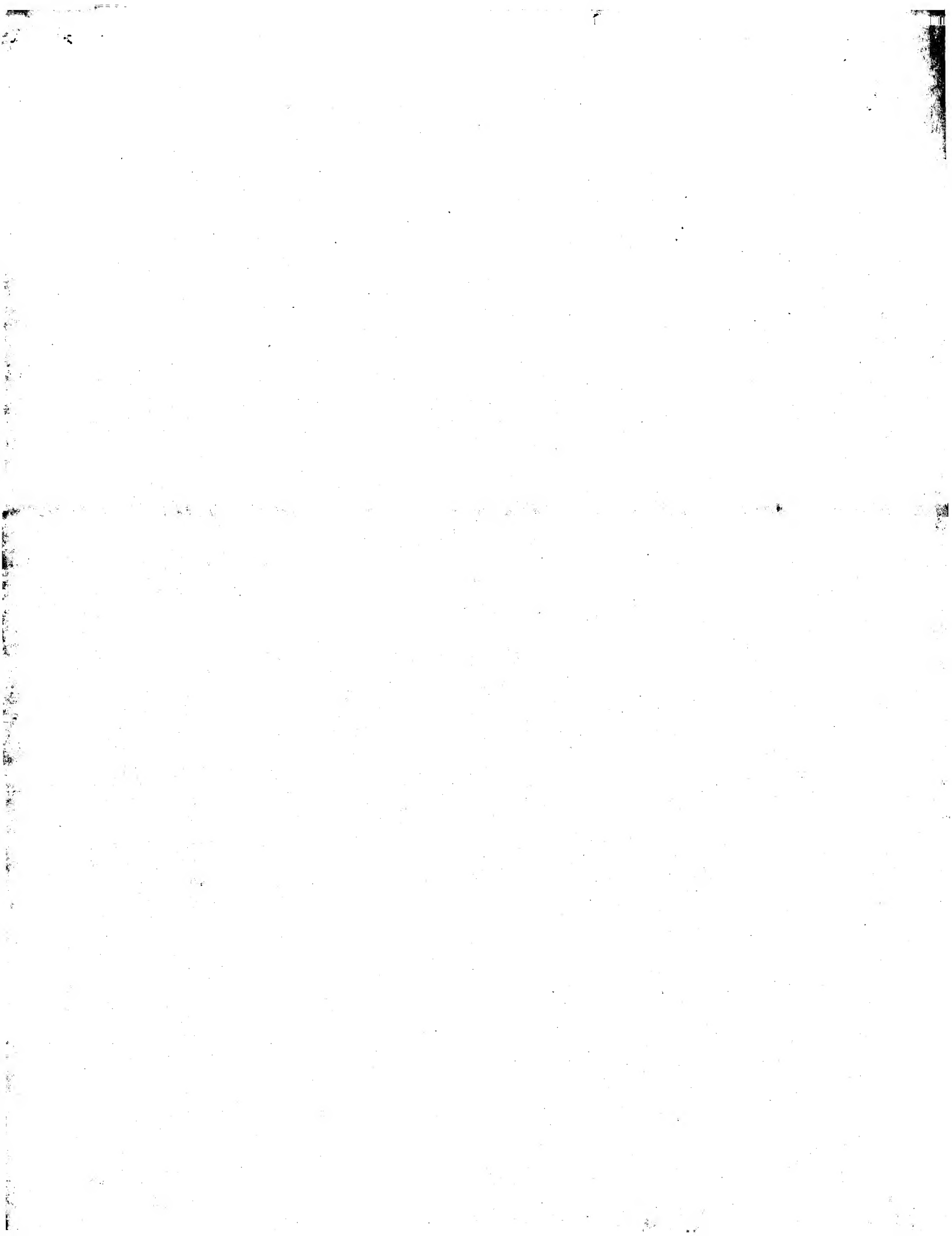
Example 4; Fig 4; 120pp; English.

This polypeptide comprise a novel human receptor tyrosine kinase
designated muscle specific kinase (Musk) that is expressed in
normal and denervated muscle. Musk is alternatively referred to
Dmk for denervated muscle kinase. The amino acid sequence was
deduced from an isolated cDNA clone (see AAT90471). Rat Musk (see
AAM26610) has also been identified. Use of Musk to generate anti-
Musk antibodies and in the diagnosis of neurological or other
disorders is disclosed. Assay systems that may be used to detect
and/or measure ligands that bind the musk gene product are provided.
A claimed method of promoting the growth, differentiation or
survival of Musk receptor-expressing cells involves administration
to the cell of agrin (see AAM26609). Such cells include muscle,
heart, spleen, ovary and retina cells, or cells genetically
engineered to express the Musk receptor.

Sequence 869 AA:

Query Match 99.8%; Score 4558; DB 18; Length 869;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MRELNIPIVHLITLVAFSGTEKLPKAPVITPTPLETVDAIVEEATFMCAVESYPOPEIS 60
1 mrelniplvhlitlvafsgteklpkapvittptpletvdaiveeatfmcavesypopeis 60
61 WTRNKILIKLFDRIYSIRENGQLITLISVEDSDGIYCTANNGVGAVESGALGVKMK 120
61 wtrnkililiklfdriysirengqlitlisedsdgiyctannvgavescgalgvkmk 120



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QY 121 PKTRPPINVKIIEGLKAVLPCTTNGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNV 180
Db 121 PKTRPPINVKIIEGLKAVLPCTTNGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNV 180
QY 181 OKEDAGOVRCVAKNSLGTAYSKVVKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
Db 181 OKEDAGOVRCVAKNSLGTAYSKVVKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
QY 241 PTTMIENGNAVSSGSIQESVDRVIDSRLOLFTFKPGLYCIATNKGEFSTAKAAAT 300
Db 241 PTTMIENGNAVSSGSIQESVDRVIDSRLOLFTFKPGLYCIATNKGEFSTAKAAAT 300
QY 301 ISIAEWSKPOKDNKGYCAOYRGECVNAVLAKDALVFLNTSYADPEAOELVHTANNEKX 360
Db 301 ISIAEWSKPOKDNKGYCAOYRGECVNAVLAKDALVFLNTSYADPEAOELVHTANNEKX 360
QY 361 VVSPVCRPAEALICNHIIFGECSPGVVPTPIPCREYCLAVKELFCAKEWLVMEKTHRG 420
Db 361 VVSPVCRPAEALICNHIIFGECSPGVVPTPIPCREYCLAVKELFCAKEWLVMEKTHRG 420
QY 421 LYREEMHLISVPCSKLPSMMDPTACARPLHLDYNNKENTKTFPPMSSKSVDPINLPS 480
Db 421 LYREEMHLISVPCSKLPSMMDPTACARPLHLDYNNKENTKTFPPMSSKSVDPINLPS 480
QY 481 SSSSFSVSPRTYSMTVTIISIMSSFAIVLTLTTLCCRRRQKQKKNKRESAAVTLTLP 540
Db 481 SSSSFSVSPRTYSMTVTIISIMSSFAIVLTLTTLCCRRRQKQKKNKRESAAVTLTLP 540
QY 541 SELLDLHPMPYORMBLLNPKLLSLFYRNNIERYROIGEGAFGVFOARAPGLLPY 600
Db 541 SELLDLHPMPYORMBLLNPKLLSLFYRNNIERYROIGEGAFGVFOARAPGLLPY 600
QY 601 EPTTMAVKMLKEBASADMOQDFOREALMAEFDPNPVILKLGCAVGKRPCLTFEYMAX 660
Db 601 EPTTMAVKMLKEBASADMOQDFOREALMAEFDPNPVILKLGCAVGKRPCLTFEYMAX 660
QY 661 GDNELFRMSRPHVCSLSHSDLSMRQVSPGPPPSGABOLCTANQVAAAYLSERK 720
Db 661 GDNELFRMSRPHVCSLSHSDLSMRQVSPGPPPSGABOLCTANQVAAAYLSERK 720
QY 721 FVHRDLATRNCLVGENNVKIAIDFGLSRNITSADYKANENDAPIRMPPESTFEYRYT 780
Db 721 FVHRDLATRNCLVGENNVKIAIDFGLSRNITSADYKANENDAPIRMPPESTFEYRYT 780
QY 781 TESVNAVYGVVLEIFESYGLQPIYGAHHEVYTYVRDGNILSCENCPVELLYNMLRCLWS 840
Db 781 TESVNAVYGVVLEIFESYGLQPIYGAHHEVYTYVRDGNILSCENCPVELLYNMLRCLWS 840
QY 841 KLPADRPSTSIHRIELRMCEBAGTYSV 869
Db 841 KLPADRPSTSIHRIELRMCEBAGTYSV 869

```

RESULT 4

AAW26506
ID AAW26506 standard; Protein; 869 AA.

AAW26506:

06-JAN-1998 (first entry)

Human Dmk receptor.

Dmk receptor: tyrosine kinase receptor; signal transduction; assay;

therapy; diagnosis; Alzheimer's disease; Parkinson's disease;

amyotrophic lateral sclerosis; Lou Gehrig's disease;

idiopathic torsion dystonia; muscle atrophy.

Homo sapiens.

US5656473-A.

12-AUG-1997.

```

XX 21-JUL-1993: 9305-0095658.
XX 19-JAN-1995: 9505-0374834.
XX 21-JUL-1993: 9305-0095658.
XX (REG-) REGENERON PHARM INC.
XX Rojas EA, Valenzuela DM;
XX WPI; 1997-414593/38.
XX N-PDB; AAT87073.
XX New isolated human denervated muscle kinase receptor - used to
XX develop products for the diagnosis and treatment of neurological,
XX muscle or neuromuscular disorders
XX Claim 4; Column 31-36; 31pp; English.

```

This polypeptide comprises the human Dmk receptor (AAW26506), a novel tyrosine kinase receptor that is expressed in high levels in denervated muscle. Its amino acid sequence was deduced from an isolated nucleic acid molecule (see AAT87073). The Dmk receptor can be used to screen for agents that interact with Dmk. Agents that bind to the receptor may mediate survival and differentiation in cells naturally expressing the receptor, but may also confer survival and proliferation when used to treat cells engineered to express the receptor. Dmk receptor polypeptides and polynucleotides can also be used for detecting abnormalities in the function or expression of the receptor which may be used in the diagnosis of muscular or other disorders. Manipulation of the receptor or agonists which bind this receptor may be used to treat neurological diseases, diseases of muscle or neuromuscular unit disorders, including Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (Lou Gehrig's disease), idiopathic torsion dystonia and muscle atrophy. The extracellular domain (ECD) of the receptor can be used to block the binding of receptor to target cells. A receptorbody comprising the ECD fused to a human Ig gamma-1 constant region is claimed.

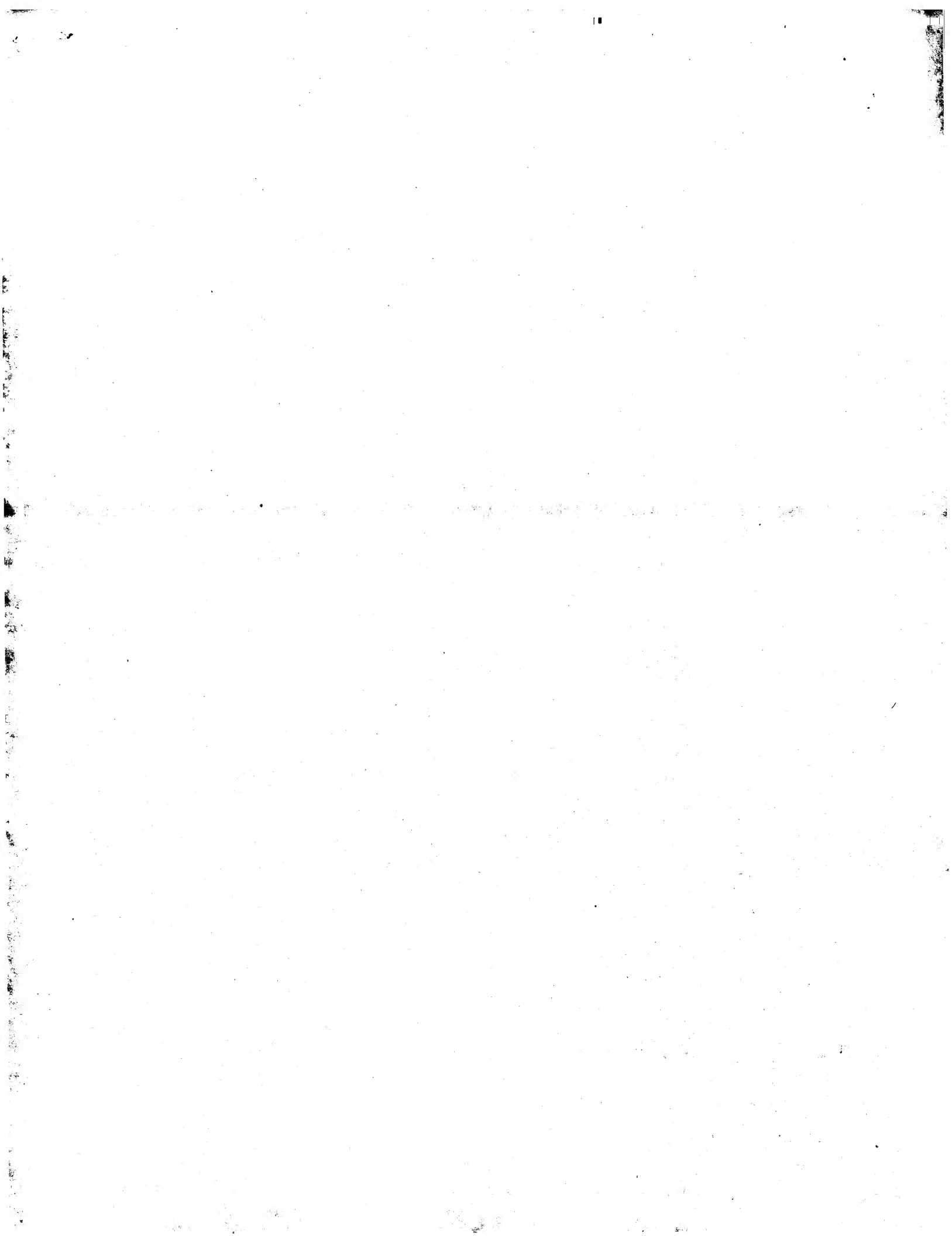
Sequence 869 AA:

Query Match 99.8%; Score 4558; DB 18; Length 869;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MRLVNIPLVHILTLVAFSTETKLPKAPYITTLLEVVDALVEVAIFMCAVESYPOPEIS 60
Db 1 MRLVNIPLVHILTLVAFSTETKLPKAPYITTLLEVVDALVEVAIFMCAVESYPOPEIS 60
QY 61 WTRNKLILKLFDRYSIRENGOLLTLLSVESDSDGTYCCANNGVGAVSGALQVKKM 120
Db 61 WTRNKLILKLFDRYSIRENGOLLTLLSVESDSDGTYCCANNGVGAVSGALQVKKM 120
QY 121 PKTRPPINVKIIEGLKAVLPCTTNGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNV 180
Db 121 PKTRPPINVKIIEGLKAVLPCTTNGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNV 180
QY 181 OKEDAGOVRCVAKNSLGTAYSKVVKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
Db 181 OKEDAGOVRCVAKNSLGTAYSKVVKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
QY 241 PTTMIENGNAVSSGSIQESVDRVIDSRLOLFTFKPGLYCIATNKGEFSTAKAAAT 300
Db 241 PTTMIENGNAVSSGSIQESVDRVIDSRLOLFTFKPGLYCIATNKGEFSTAKAAAT 300
QY 301 ISIAEWSKPOKDNKGYCAOYRGECVNAVLAKDALVFLNTSYADPEAOELVHTANNEKX 360
Db 301 ISIAEWSKPOKDNKGYCAOYRGECVNAVLAKDALVFLNTSYADPEAOELVHTANNEKX 360
QY 361 VVSPVCRPAEALICNHIIFGECSPGVVPTPIPCREYCLAVKELFCAKEWLVMEKTHRG 420
Db 361 VVSPVCRPAEALICNHIIFGECSPGVVPTPIPCREYCLAVKELFCAKEWLVMEKTHRG 420

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OY 421 LYRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNENLKTPEPMTSKPSVDIPNLS 480
DB 421 LYRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNENLKTPEPMTSKPSVDIPNLS 480
OY 481 SSSSSFSVSPYSMVTYISIMSSFAIFVLLITTLVCCRRRQWKKKRESAAVTLTLP 540
DB 481 SSSSSFSVSPYSMVTYISIMSSFAIFVLLITTLVCCRRRQWKKKRESAAVTLTLP 540
OY 541 SELLDRLHPNMYQRMPLLNPKLLSLEYPRNNIEYRDIGEGAFGVQARAPGLLP 600
DB 541 SELLDRLHPNMYQRMPLLNPKLLSLEYPRNNIEYRDIGEGAFGVQARAPGLLP 600
OY 601 EPTTVAVVKMLKEASADMDQADFORAALMAEFDNPNIVKLLGVCAVGRPMCLLFEMAY 660
DB 601 EPTTVAVVKMLKEASADMDQADFORAALMAEFDNPNIVKLLGVCAVGRPMCLLFEMAY 660
OY 661 GDLMELFRSMSPHVCISHSDDLKRAVSSPPPPSLCAQDLCTAROVAAGMAYLSERK 720
DB 661 GDLMELFRSMSPHVCISHSDDLKRAVSSPPPPSLCAQDLCTAROVAAGMAYLSERK 720
OY 721 FVHDLATRNCLVGENMYKADFGLSNRYSDAYKANENDAIPIRMPESTIFYNRYT 780
DB 721 FVHDLATRNCLVGENMYKADFGLSNRYSDAYKANENDAIPIRMPESTIFYNRYT 780
OY 781 TESQVMAVGVVLMETSYGLOPYGMAHEEVIYVRDGNILSCPEVPELYNLMRLCWS 840
DB 781 TESQVMAVGVVLMETSYGLOPYGMAHEEVIYVRDGNILSCPEVPELYNLMRLCWS 840
OY 841 KLPAKPSFMSIHRIERMCERAGTYSV 869
DB 841 KLPAKPSFMSIHRIERMCERAGTYSV 869

RESULT 5
ID AAM26610 standard; protein; 868 AA.
AC AAM26610;
XX 27-JAN-1998 (first entry)
DE Rat muscle-specific kinase (Musk).
XX Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; rat;
XX ligand; agrin; diagnosis; therapy.
XX Rattus sp.
FH Key Location/Qualifiers
FT Peptide 1..19
FT Domain /label= Sig_peptide 21..492
FT Domain /label= Extracellular_domain 493..521
FT Domain /label= Transmembrane_domain 522..868
FT Domain /label= Intracellular_domain

MO9721811-A2.
XX 19-JUN-1997.
XX 13-DEC-1996; 96MO-0520696.
XX 10-MAY-1996; 96US-0644371.
XX 15-DEC-1995; 95US-0008657.
XX (REGG-) REGENERON PHARM INC.
XX Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD:
XX WPI, 1997-332783/30.

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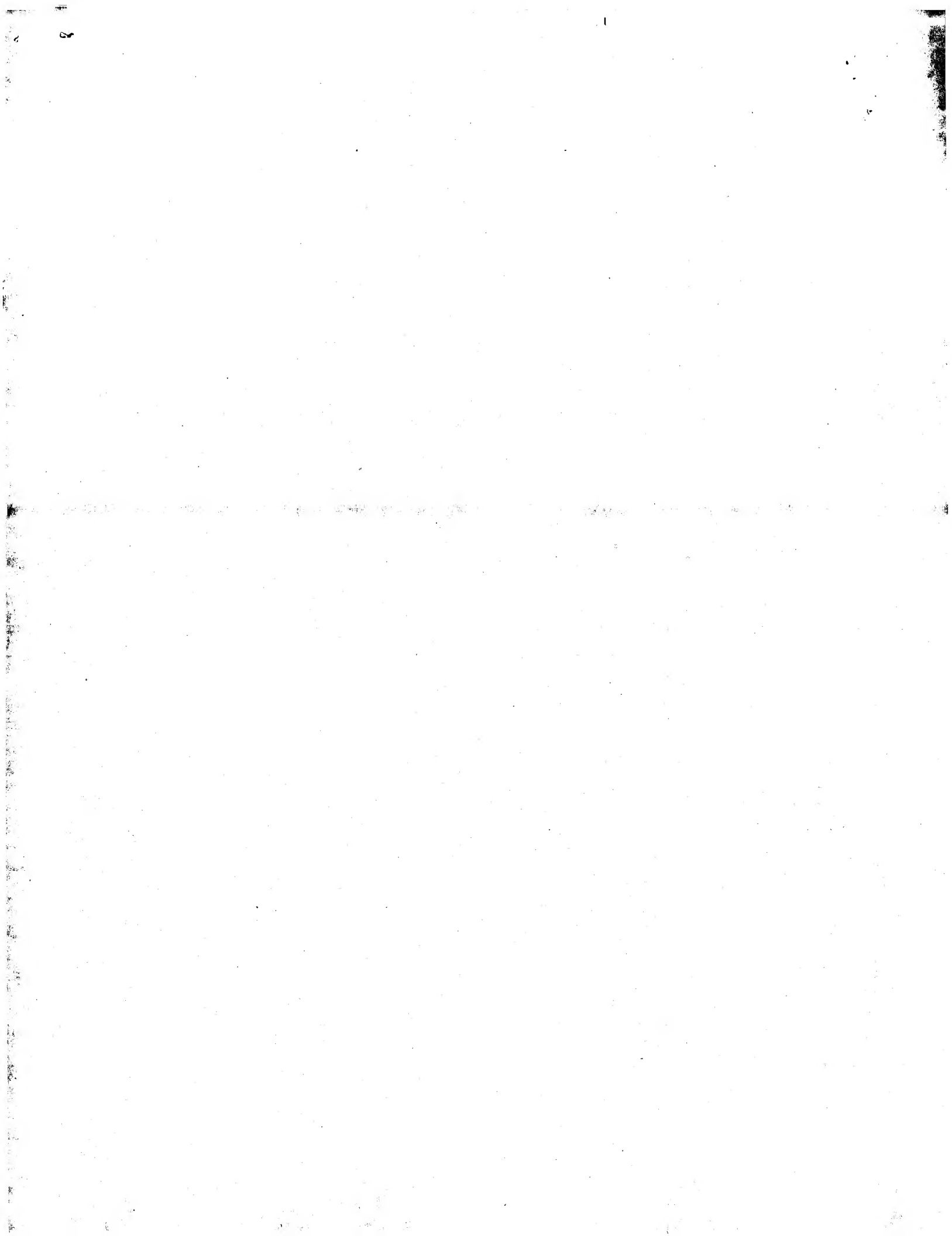
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DR N-PSDB: AAT90472.
XX Nucleotide sequences encoding human agrin and muscle specific kinase
PT and related receptor - used in diagnosis and treatment of disorder
PT with muscle atrophy
XX
PS Example 1; Fig 1; 120pp; English.
XX
CC This polypeptide comprise a novel rat receptor tyrosine kinase
CC designated muscle specific kinase (Musk) that is expressed in
CC normal and denervated muscle. Musk is alternatively referred to
CC Dmk for denervated muscle kinase. The amino acid sequence was
CC deduced from an isolated cDNA clone (see AAT90472). Human Musk (see
CC AAM26611) has also been identified. Use of Musk to generate anti-
CC Musk antibodies and in the diagnosis of neurological or other
CC disorders is disclosed. Assay systems that may be used to detect
CC and/or measure ligands that bind the musk gene product are provided.
CC A claimed method of promoting the growth, differentiation or
CC survival of Musk receptor-expressing cells involves administration
CC to the cell of agrin (see AAM26609). Such cells include muscle,
CC heart, spleen, ovary and retina cells, or cells genetically
CC engineered to express the Musk receptor.
XX
SQ Sequence 868 AA:

Query Match 93.9%; Score 4292.5; DB 18; Length 868.
Best Local Similarity 93.2%; Pred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

OY 1 MRELVINPIVLHITLVAFSGTEKLPKAPVTTTPEYTDALVEEVAFMCAVESYPOEIS 60
DB 1 mrelvinpilhmtlvaifsgeklpkapvtttpleytdalveevafmcavesypdpels 60
OY 61 WTRNKILIKLFDTRYISIRENGQLITLLSVBDSDDGIYCTANNVGAVESGALQYKMK 120
DB 61 wtrnkililkfdtryisirengqlitllsvbdsddgiyctannvgavescgalqykkm 120
OY 121 PKITRPINVKILIEGLKAVLPCTTGNPKPSVMIKGDSPLENSRIKAVLESGSLRIHNV 180
DB 121 pkitrpinvkiileglkavlpcttgnpkpsvwmikgdsplensriavlesgslrihmv 180
OY 181 QKEDAGQRCVAAKNSLTATSKVYKLEFEVFAILRLAPESHNATFGSFVRLHGTATGIPV 240
DB 181 qkedagqrcvvaaknsltatskvylklefevfaillrlapeshnatfgsfvrlhgtatgipv 240
OY 241 PTTTWIENGNAVSSGSIQESVKDVIDSRQLPFTIRPGLYTCIATNKGKFEFTAKAAAT 300
DB 241 pttwiengnavssgsiqesvkdrvidsrqlpftirpglytciatnkgkfstakaaat 300
OY 301 ISIAEMSKPKDKMGYCAQVRGEVCNAVLAKDALVFLNTSYADPEERQELLVHTANNEK 360
DB 301 isiaemskpkdkmgycavrgvcnavlakdalvflntsyadpeerqellvhtannek 360
OY 361 VSLAEWSKSKESKYGCAQYRGVCDALVYKSLVFTNTPYDPEEQELLHITLAVNELK 360
DB 361 vslaeWSKSKESKYGCAQYRGVCDALVYKSLVFTNTPYDPEEQELLHITLAVNELK 360
OY 361 VSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKENVLVEEKTHRG 420
DB 361 vspvcrpaEallcnhifqecspgvvptpiPCREYCLAVKELFCAKENVLVEEKTHRG 420
OY 421 LYRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNENLKTPEPMTSKPSVDIPNLS 480
DB 421 LYRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNENLKTPEPMTSKPSVDIPNLS 480
OY 481 SSSSSFSVSPYSMVTYISIMSSFAIFVLLITTLVCCRRRQWKKKRESAAVTLTLP 540
DB 481 SSSSSFSVSPYSMVTYISIMSSFAIFVLLITTLVCCRRRQWKKKRESAAVTLTLP 540
OY 541 SELLDRLHPNMYQRMPLLNPKLLSLEYPRNNIEYRDIGEGAFGVQARAPGLLP 600
DB 541 SELLDRLHPNMYQRMPLLNPKLLSLEYPRNNIEYRDIGEGAFGVQARAPGLLP 600
OY 601 EPTTVAVVKMLKEASADMDQADFORAALMAEFDNPNIVKLLGVCAVGRPMCLLFEMAY 660
DB 601 EPTTVAVVKMLKEASADMDQADFORAALMAEFDNPNIVKLLGVCAVGRPMCLLFEMAY 660

```



QY 661 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPPGPLSCAEOLCIARQVAAAGMAYLSERK 720
 Db 660 gdlneflrsmshphtvcslshsdlsstrarvssppgpplscaeqlclarqvaagmaylsesrk 719
 QY 721 FVHRDLATRNCLVGENMVKVITADFGLSRNIYSADYKANKANDAIPIRMMPPESTFYNNRT 780
 Db 720 fvhrdlatrncldvgenmvkltadfglsrnllysadylkagndalpiirmmppestfynrtyt 779
 QY 781 TESDVWAVGVVLMWEIFSYGLQPYRGMAHEEVIYVRDGNILSCPENCPVELYNMRLCWS 840
 Db 780 tesdvwavgvvlmwelfsyglqpyrgmaheevlyyvrdsnllacpencpvelynmlrclws 839
 QY 841 KLPA DRPSTSIHRLIERMRCERAEGVSV 869
 Db 840 klpadrpsfcsihrlirmceraegetvgy 868

RESULT 6

AAW26507
 AAW26507 standard; Protein: 868 AA.

AAW26507;

06-JAN-1998 (first entry)

Rat Dmk receptor.

Dmk receptor; tyrosine kinase receptor; signal transduction; assay; therapy; diagnosis.

Rattus sp.

Key Location/Qualifiers

Peptide 1..19

Domain /label= Sig.peptide

Domain /label= Extracellular

Domain /label= Transmembrane

Domain /label= Intracellular

US5656473-A.

12-AUG-1997.

21-JUL-1993; 93US-0095658.

19-JAN-1995; 95US-0374834.

21-JUL-1993; 93US-0095658.

(REGE-) REGENERON PHARM INC.

Rojas EA, Valenzuela DM;

WPI; 1997-414593/38.

N-PSDB; AAT87074.

New isolated human denervated muscle kinase receptor - used to develop products for the diagnosis and treatment of neurological, muscle or neuromuscular disorders

Example 1; Column 19-24; 31p; English.

This polypeptide sequence comprises the rat Dmk receptor, a novel tyrosine kinase receptor that is expressed at high levels in denervated muscle. Its amino acid sequence was deduced from an isolated cDNA clone (see AAT87074). Human Dmk receptor (see AAW26506) has also been identified and can be used to develop products for the diagnosis and treatment of neurological, muscle or neuromuscular disorders.

SQ Sequence 868 AA:

Query Match 93.9%; Score 4292.5; DB 18; Length 868;

Best Local Similarity 93.2%; Pred. No. 0;

Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

QY 1 MRELNVNIPVLHILITVAAGTEKLEPKAPVITPTLETVDAIVEVATFMCAVESYPOPEIS 60
 Db 1 mrelnvnpilgmlltvalasgtekllpkapvitptletvdalveevatfmcavesypopels 60
 QY 61 WTRNKILIKLEFTRYSIRBNQGLTILSVEDSDGITYCTANNGVGAESGALQVKKR 120
 Db 61 wtrnkililkfetrysirengqlltilsvededgityctannvggavesgalqvkk 120
 QY 121 PRTTPPIVNVKILIEGLKAVLPCTTMGNKRPSPVSKGSPLENRNRIAVLEGSLRIHV 180
 Db 121 prttrppilnvkilleglkavlpcttmgnkpsvskgsprenrnriavlegslrihv 180
 QY 181 OKEDAGQYRCVAKNSLGTAVYSKVVLKEFEVFAIRIRAPESHNVTFGSFVTLHCTATGIPV 240
 Db 181 okedagqyrcvaknslgtavyskvvlkefevfarirapeshnvtfgsfvtlhtctatgipv 240
 QY 241 PTTIENGNAVSSGSIQESYKDRVIDSRLOLFTKPGLYTCIAQNKGEKSTAKAAT 300
 Db 241 pttiengnavssgsiqesykdrrvidsrloqlftkpglytciaqnkgekstakaaat 300
 QY 301 ISIAEMSKPQKNGCYCAOYRGECNNAVLDALVFLTSTVADPEAOELVHTANELK 360
 Db 301 isiaemskpqkngcycaoyrgecnnavldalvflstvadpeaoelvhtanelk 360
 QY 361 VVSPVCRPAEALICNHIIFQECSPGVPTPIPCREYICLAVELCAKEMLVMEKETHG 420
 Db 361 vvspvcrpaeealichnhiifqecspgvptpicreyiclavvelcakemlvmekehtg 420
 QY 421 LYRSMHLISVPKCKSLPSMHWDPACARLPHLDYKNENLTFPPMTSSKSPVDIPNDPS 480
 Db 421 lyrsmhllisvpkckslpsmhwdpacarlphldyknenltpfpmstsskspvdipndps 480
 QY 481 SSSSEFSYSPYSMVITISISSFAIFLITITLYCCRRKROKMKRESAAVLTLP 540
 Db 481 ssssefsyspysmvitisissfaiflittitlyccrrrkrokmkresaaavltp 540
 QY 541 SELLDRLHPNMYQRMPLINPKLLSLEYPRNNIEYRDIGEGAFGVFORARAGLLPY 600
 Db 540 sellldrlhpnmymqrmpllnpkllsleyprnnieyrdigegafgvforaragllpy 600
 QY 601 EPTWVAVKMLEEASADMDQADFOREALMAEFDPNIVTKLGVCAVGRPKMCLFEYNAY 660
 Db 601 eptwvavkmleeasadmddqadforealmaefdpnivtklgvcavgrpkmcclfeynay 660
 QY 660 eptwvavkmleeasadmddqadforealmaefdpnivtklgvcavgrpkmcclfeynay 660
 QY 661 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPPGPLSCAEOLCIARQVAAAGMAYLSERK 720
 Db 660 gdlneflrsmshphtvcslshsdlsstrarvssppgpplscaeqlclarqvaagmaylsesrk 719
 QY 721 FVHRDLATRNCLVGENMVKVITADFGLSRNIYSADYKANKANDAIPIRMMPPESTFYNNRT 780
 Db 720 fvhrdlatrncldvgenmvkltadfglsrnllysadylkagndalpiirmmppestfynrtyt 779
 QY 781 TESDVWAVGVVLMWEIFSYGLQPYRGMAHEEVIYVRDGNILSCPENCPVELYNMRLCWS 840
 Db 780 tesdvwavgvvlmwelfsyglqpyrgmaheevlyyvrdsnllacpencpvelynmlrclws 839
 QY 841 KLPA DRPSTSIHRLIERMRCERAEGVSV 869
 Db 840 klpadrpsfcsihrlirmceraegetvgy 868

RESULT 7

AAW92717

ID AAW92717 standard; Protein: 868 AA.

AAW92717;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2002, 13:36:00 ; Search time 37.92 Seconds

(without alignments)
3964.467 Million cell updates/sec

Title: US-09-817-487a-2

Sequence: 1 MRLVNIPLVHILVAFSG.....TSIHRIERMCERAEIVSV 869

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 1000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: SP archaea
2: SP bacteria
3: SP fungi
4: SP human
5: SP invertebrate
6: SP mammal
7: SP mhc
8: SP organelle
9: SP phage
10: SP plant
11: SP rodent
12: SP virus
13: SP vertebrate
14: SP unclassified
15: SP virus
16: SP bacteriophage
17: SP archaea

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	4292.5	93.9	868	11	062838
3	4269.5	93.4	868	11	061006
4	4220.5	92.4	860	11	061005
5	4136	90.5	871	11	061987
6	4128	90.3	881	11	061988
7	2897	63.4	946	13	007153
8	1602	35.1	724	5	09VDA2
9	1129.5	24.7	1145	5	09V6K3
10	966.5	21.2	821	13	09V6K8
11	802	17.5	811	13	09VH44
12	792.5	17.3	839	4	075682
13	778	17.0	685	5	024488
14	773.5	16.9	928	5	09B171
15	772	16.9	902	5	017576

17	754.5	16.5	591	4	015656	015656 homo sapien
18	750.5	16.4	790	13	090699	090699 gallus gall
19	740.5	16.2	503	4	015655	015655 homo sapien
20	738.5	16.2	486	13	09P579	09P579 xenopus lae
21	724.5	15.9	802	13	042127	042127 xenopus lae
22	720	15.8	782	11	061563	061563 mus musculu
23	720	15.8	796	13	091287	091287 pleurodeles
24	720	15.8	972	5	026614	026614 strongyloce
25	715	15.6	800	4	09052	09052 homo sapien
26	712	15.6	800	4	09052	09052 homo sapien
27	709	15.6	800	13	091373	091373 xenopus tr
28	708	15.5	800	11	09JHX9	09JHX9 rattus norv
29	705.5	15.4	922	13	090413	090413 brachydanio
30	702.5	15.4	814	13	091897	091897 xenopus lae
31	697.5	15.3	850	6	09SM13	09SM13 bos taurus
32	686.5	15.2	650	11	063709	063709 rattus rat
33	685.5	15.2	800	13	09P596	09P596 xenopus lae
34	690.5	15.1	989	13	09P183	09P183 brachydanio
35	686.5	15.0	824	13	09P186	09P186 gallus gall
36	681	14.9	766	4	090749	090749 gallus gall
37	681	14.9	766	4	096KM2	096KM2 homo sapien
38	681	14.9	766	4	096KM1	096KM1 homo sapien
39	679	14.9	819	4	096KM0	096KM0 homo sapien
40	677	14.8	822	11	060818	060818 mus musculu
41	676	14.8	876	11	060752	060752 mus musculu
42	676	14.8	782	6	09TW23	09TW23 oryctolagus
43	672	14.7	806	13	090200	090200 brachydanio
44	670	14.7	609	13	091776	091776 xenopus lae
45	670	14.7	1362	13	09PV24	09PV24 xenopus lae

ALIGNMENTS

RESULT 1
ID 015146 PRELIMINARY; PRT: 869 AA.
AC 015146;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MUSCLE SPECIFIC TYROSINE KINASE RECEPTOR.
GN MUSK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-96009854; PubMed-7546737;
RA Valenzuela D.M., Stilt T.N., Stefano P.S., Rojas E., Mattson K.,
RA Compton D.L., Nunez L., Park J.S., Stark J.L., Gies D.R., Thomas S.,
RA Lebeau M.M., Fernald A.A., Copeland N.G., Jenkins N.A., Burden S.J.,
RA Glass D.J., Yancopoulos G.D.;
RT "Receptor tyrosine kinase specific for the skeletal muscle lineage:
RT expression in embryonic muscle, at the neuromuscular junction, and
RT after injury";
RT Neuron 15:573-584(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Valenzuela D.M., Rojas E., Yancopoulos G.D.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RA EMBL: AF006464; AAB63044.1;
DR HSSP: P11362; IPKG.
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR000719; Euk_PKinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001245; Tyr_PKinase.
DR Pfam: PF01392; Fz_1.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF00069; pkinase; 1.

PRINTS; PRO0109; TYRKINASE.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00219; TYKIC; 1.
 DR PROSITE; PS50038; F2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
 DR ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
 KW Tyrosine-protein kinase.
 SQ SEQUENCE 869 AA; 97056 MW; 3DDC20E179FA010C CRC64;

Query Match 99.8%; Score 4558; DB 4; Length 869;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MRELVIPLVHILTLVAFSGTEKLPKAPVITPLEVDALVEEATFMCAYESYPOETS 60
 1 MRELVIPLVHILTLVAFSGTEKLPKAPVITPLEVDALVEEATFMCAYESYPOETS 60
 61 WTRNKLILKLFTRYSIRENGQLTILSVESDDGTYCCTANNGVGAVERSCALQVKK 120
 61 WTRNKLILKLFTRYSIRENGQLTILSVESDDGTYCCTANNGVGAVERSCALQVKK 120
 121 PRTTPIVAVKIIIEGKAVLPCTTGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNY 180
 121 PRTTPIVAVKIIIEGKAVLPCTTGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNY 180
 181 QKEDAGQYRCVAKNSLGTAYSKVVKLEFVFAIILAPESHVNTGSEFTLHCTATGIV 240
 181 QKEDAGQYRCVAKNSLGTAYSKVVKLEFVFAIILAPESHVNTGSEFTLHCTATGIV 240
 181 QKEDAGQYRCVAKNSLGTAYSKVVKLEFVFAIILAPESHVNTGSEFTLHCTATGIV 240
 241 PRTTPIVAVKIIIEGKAVLPCTTGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNY 180
 241 PRTTPIVAVKIIIEGKAVLPCTTGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNY 180
 301 ISIAEMSKPKONKGYCQYREGVNAVILAKALVFLNTSYADPEADQLVHTAMNBLK 360
 301 ISIAEMSKPKONKGYCQYREGVNAVILAKALVFLNTSYADPEADQLVHTAMNBLK 360
 301 ISIAEMSKPKONKGYCQYREGVNAVILAKALVFLNTSYADPEADQLVHTAMNBLK 360
 361 VVSPVCRPAEALCNHIFOECSPEVVPPIPIREYCLAVKELCAEMVMEKTRHG 420
 361 VVSPVCRPAEALCNHIFOECSPEVVPPIPIREYCLAVKELCAEMVMEKTRHG 420
 421 LYRSEMHLISVPCSKLSESHMDPACARLPHLDYKNENLKTFFPMTSSKPSVDIPNLS 480
 421 LYRSEMHLISVPCSKLSESHMDPACARLPHLDYKNENLKTFFPMTSSKPSVDIPNLS 480
 481 SSSSFVSPTYSMTVIISISSFAIFLITLTYCCRRKKOKKKRESAAVTLTLP 540
 481 SSSSFVSPTYSMTVIISISSFAIFLITLTYCCRRKKOKKKRESAAVTLTLP 540
 481 SSSSFVSPTYSMTVIISISSFAIFLITLTYCCRRKKOKKKRESAAVTLTLP 540
 541 SELLDLHLHPNPMYQRPMLLNPRLSLEYPRNNIEYRDIGEGAFGRVQARAPGLLP 600
 541 SELLDLHLHPNPMYQRPMLLNPRLSLEYPRNNIEYRDIGEGAFGRVQARAPGLLP 600
 601 EPTTMAVVKLKEEASADMDQADPQREALAEFNPNTIKLGVCAVAKPKCFLFEYMA 660
 601 EPTTMAVVKLKEEASADMDQADPQREALAEFNPNTIKLGVCAVAKPKCFLFEYMA 660
 661 GDNIEFLRSMPTVCSLSHSDLSMAQVSSPGPPPLSCAEQICINQVAAAGNATYSEK 720
 661 GDNIEFLRSMPTVCSLSHSDLSMAQVSSPGPPPLSCAEQICINQVAAAGNATYSEK 720
 721 FVHRDLATRCVLENNVYKIAFGLSRNITYSADYTKANENDAIPIRMPPESEIFNRT 780
 721 FVHRDLATRCVLENNVYKIAFGLSRNITYSADYTKANENDAIPIRMPPESEIFNRT 780
 781 TESDVAAVGVLEIRISYGLQPYGMAHEVITYYVDGNILSPENCYVELYIMRLCMS 840
 781 TESDVAAVGVLEIRISYGLQPYGMAHEVITYYVDGNILSPENCYVELYIMRLCMS 840

QY 841 KLPADRPSTIRILERMCEAGETVSV 869
 DB 841 KLPADRPSTIRILERMCEAGETVSV 869

RESULT 2
 ID 062838 PRELIMINARY; PRT: 868 AA.
 AC 062838;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE MOLECULE-SPECIFIC TYROSINE KINASE RECEPTOR MUSK.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI-TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96009854; PubMed=7546737;
 RA Valenzuela D.M., Stitt T.N., Stefano P.S., Rojas E., Mattson K.,
 RA Compton D.L., Nunez L., Park J.S., Stark J.L., Gles D.R., Thomas S.,
 RA Lebeau M.M., Bernad A.A., Copeland N.G., Jenkins N.A., Burden S.J.,
 RA Glass D.J., Yacopoulos G.D.;
 RT "Receptor tyrosine kinase specific for the skeletal muscle lineage:
 RT expression in embryonic muscle, at the neuromuscular junction, and
 RT after injury";
 RL Neuron 15:573-584 (1995).
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC EMBL: U34985; AAA0956.1;
 DR HSSP: P1362; IIGK.
 DR InterPro: IPR002453; beta_tubulin.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000024; F2_domain.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR00306; Ig_MHC.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Ser_thr_pkinase.
 DR Pfam: PF01392; F2; 1.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PRO0109; TYRKINASE.
 DR SMART: SM00408; IGC2; 3.
 DR SMART: SM00219; TYKIC; 1.
 DR PROSITE: PS50038; F2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
 DR ATP-binding; Immunoglobulin domain; Kinase; Receptor;
 KW Serine/threonine-protein kinase; Transferase;
 SQ SEQUENCE 868 AA; 96821 MW; C16B4E74EE25B24 CRC64;

Query Match 93.9%; Score 4292.5; DB 1; Length 868;
 Best Local Similarity 93.2%; Pred. No. 0;
 Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

1 MRELVIPLVHILTLVAFSGTEKLPKAPVITPLEVDALVEEATFMCAYESYPOETS 60
 1 MRELVIPLVHILTLVAFSGTEKLPKAPVITPLEVDALVEEATFMCAYESYPOETS 60
 61 WTRNKLILKLFTRYSIRENGQLTILSVESDDGTYCCTANNGVGAVERSCALQVKK 120
 61 WTRNKLILKLFTRYSIRENGQLTILSVESDDGTYCCTANNGVGAVERSCALQVKK 120
 121 PRTTPIVAVKIIIEGKAVLPCTTGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNY 180
 121 PRTTPIVAVKIIIEGKAVLPCTTGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNY 180
 181 QKEDAGQYRCVAKNSLGTAYSKVVKLEFVFAIILAPESHVNTGSEFTLHCTATGIV 240
 181 QKEDAGQYRCVAKNSLGTAYSKVVKLEFVFAIILAPESHVNTGSEFTLHCTATGIV 240

CC method uses a mutated PKR nucleic acid which comprises a modification
 CC to the intracellular and extracellular domains, or comprises a
 CC modification to the intracellular domain and excludes any nerve growth
 CC factor receptor(s) (NGF). The method uses mutated PKR as a cell
 CC surface marker, and is useful for identifying genetically modified cells,
 CC especially immunoselection of transduced mammalian cells, and for
 CC identifying mammalian cells expressing a protein of interest. The
 CC genetically modified cells may be used in an autologous or
 CC allogeneic setting e.g. gene therapy for bone marrow transplants, graft
 CC facilitation or immune reconstitution.

XX Sequence 869 AA:

Query Match 100.0%; Score 4569; DB 22; Length 869;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MRELNVPLVHLTLVAFSGTEKLPKAPVITTPLETVDAIVEEATFMCAYESYQPEIS 60
 1 mrelvnlplvhltlvafsgteklpkapvittpletvdaiveeatfmcavesypqpeis 60
 Db 1 mrelvnlplvhltlvafsgteklpkapvittpletvdaiveeatfmcavesypqpeis 60

OY 61 WTRNKILIKLFDTRYSTIRENGQLTILSVESDDGIYCTANNVGAVESGALQVKNK 120
 61 wtrnkililkfdrystirengqltillsvedsdgiyctannvgavesgalsqvk 120
 Db 61 wtrnkililkfdrystirengqltillsvedsdgiyctannvgavesgalsqvk 120

OY 121 PKITRPINVKIIEGLKAVLPCTMGNPSPVSWIKGDSPLRENSRIANLESGRIRHNV 180
 121 pkitrpinvkiieglkavlpctmgnpvswikgdsplrensrilanlesgrirh 180
 Db 121 pkitrpinvkiieglkavlpctmgnpvswikgdsplrensrilanlesgrirh 180

OY 181 OKEDAGQRCVAKNSLGTAYSKVKEEFEPARILRAPESHNVTGSEFVTLHCTATGIPV 240
 181 okedagqrcvaknslgtayskvkeefeparilrapeshnvtgsefvtlhcta 240
 Db 181 okedagqrcvaknslgtayskvkeefeparilrapeshnvtgsefvtlhcta 240

OY 241 PRTIENGNAVSSGSIQESVADRIDSRLOLFTKPGIYTCIATNKHGEKSTAKAAT 300
 241 prtiengnavssgsiqesvadridsrloqlftrkpgiyltciatnkhgksta 300
 Db 241 prtiengnavssgsiqesvadridsrloqlftrkpgiyltciatnkhgksta 300

OY 301 ISIAEMSKPOKNGKYCAQYRGECVNAVAKDALVFLNLSVADPREAOELIHTAMNEIK 360
 301 isiaemskpokngkycaqyrgecvnavakdalvflnlsvadpreaoelihta 360
 Db 301 isiaemskpokngkycaqyrgecvnavakdalvflnlsvadpreaoelihta 360

OY 361 VVSPVCPRAAEALCNHIFQECSPGVPTPIPCREYCLAVELFCAKEMLVNEEKTHRG 420
 361 vvspvcprraealcnhifqecspgvptpircreyclavelfcakemlvneek 420
 Db 361 vvspvcprraealcnhifqecspgvptpircreyclavelfcakemlvneek 420

OY 421 LYRSMHLISVPKCKSLPSMHMDPTACARPLHDYNKENLKTFFPMWTSKSPVDIPNLS 480
 421 lyrsmhlisvpkckslpsmhmdptacarplhdynkenlktffpmwtskspv 480
 Db 421 lyrsmhlisvpkckslpsmhmdptacarplhdynkenlktffpmwtskspv 480

OY 481 SSSSFSFSPYSMVTIISMSFAIFVLTITTLCCRRKQWKNKRESAAVLTMP 540
 481 ssssfspfysmvtiismsfaifvltittlccrrkqwnkresaaavltmp 540
 Db 481 ssssfspfysmvtiismsfaifvltittlccrrkqwnkresaaavltmp 540

OY 541 SELLDRLHPNPMYOMPLLNPKLISLEYPRNNIEYVDIGEGAFGRVQARAGILPY 600
 541 sellldrlhpnpmympllnpklisleypnnieyvdigegafgrvqaragil 600
 Db 541 sellldrlhpnpmympllnpklisleypnnieyvdigegafgrvqaragil 600

OY 601 EPFTVAVAKMLKEEASADMOADFORBALMAEPDNPNIYKLGCAVCKPMLFEYMAV 660
 601 epftvavakmlkeeasadmoadforbalmepdnpniykgcavckpmlfeym 660
 Db 601 epftvavakmlkeeasadmoadforbalmepdnpniykgcavckpmlfeym 660

OY 661 GDLNEFLMSPHVTCSTSHSDLSMRAYSSGPPPLSCABOLICARQVAAAMATLSERK 720
 661 gdlneflmsphvtcstshsdlsmrayspgppplscabolicarqvaaamat 720
 Db 661 gdlneflmsphvtcstshsdlsmrayspgppplscabolicarqvaaamat 720

OY 721 FVHRDLATRNCLVGENMYVKKIADFGISRNISADYYKANENDAIPIRMWPEPSIYNYRT 780
 721 fvhrdlatrnclvgenmyvkkiadfgisrnisadyykanendaipirmwpep 780
 Db 721 fvhrdlatrnclvgenmyvkkiadfgisrnisadyykanendaipirmwpep 780

OY 781 TESDVMAAGVVLMEFSGLOPYGMAHEEVYIYRDGNIISCPENCPEVETLNLKRLCS 840
 781 tesdvmaagvvlmefsglopygmaheevyiyrdgniiscpencpevetlnl 840
 Db 781 tesdvmaagvvlmefsglopygmaheevyiyrdgniiscpencpevetlnl 840

OY 841 KLPADEPSTSIHRIIERMCEAEGTSVY 869
 841 klpadepstsihriiermceagtsvy 869
 Db 841 klpadepstsihriiermceagtsvy 869

RESULT 3
 AAM26611
 ID. AAM26611 standard; Protein: 869 AA.

AC AAM26611;

DT 27-JAN-1998 (first entry)

DE Human muscle-specific kinase (Musk).

KW Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; human.
 ligand; agrin; diagnosis; therapy.

OS Homo sapiens.

PN W09721811-A2.

PD 19-JUN-1997.

PF 13-DEC-1996; 96WO-US20696.

PR 10-MAY-1996; 96US-0644271.

PR 15-DEC-1995; 95US-0008657.

PA (REG-) REGENERON PHARM INC.

PI Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;

DR WPI: 1997-332783/30.

DX N-PSDB; AAT90473.

PT Nucleotide sequences encoding human agrin and muscle specific kinase
 PT and related receptor - used in diagnosis and treatment of disorder
 PT with muscle atrophy

PS Example 4; Fig 4; 120pp; English.

CC This polypeptide comprise a novel human receptor tyrosine kinase
 CC designated muscle specific kinase (Musk) that is expressed in
 CC normal and denervated muscle. Musk is alternatively referred to
 CC Dmk for denervated muscle kinase. The amino acid sequence was
 CC deduced from an isolated cDNA clone (see AAT90471). Rat Musk (see
 CC AAM26610) has also been identified. Use of Musk to generate anti-
 CC Musk antibodies and in the diagnosis of neurological or other
 CC disorders is disclosed. Assay systems that may be used to detect
 CC and/or measure ligands that bind the musk gene product are provided.
 CC A claimed method of promoting the growth, differentiation or
 CC survival of Musk receptor-expressing cells involves administration
 CC to the cell of agrin (see AAM26609). Such cells include muscle,
 CC heart, spleen, ovary and retina cells, or cells genetically
 CC engineered to express the Musk receptor.

XX Sequence 869 AA;

Query Match 99.8%; Score 4558; DB 18; Length 869;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MRELNVPLVHLTLVAFSGTEKLPKAPVITTPLETVDAIVEEATFMCAYESYQPEIS 60
 1 mrelvnlplvhltlvafsgteklpkapvittpletvdaiveeatfmcavesypqpeis 60
 Db 1 mrelvnlplvhltlvafsgteklpkapvittpletvdaiveeatfmcavesypqpeis 60

OY 61 WTRNKILIKLFDTRYSTIRENGQLTILSVESDDGIYCTANNVGAVESGALQVKNK 120
 61 wtrnkililkfdrystirengqltillsvedsdgiyctannvgavesgalsqvk 120
 Db 61 wtrnkililkfdrystirengqltillsvedsdgiyctannvgavesgalsqvk 120


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OY 121 PKTRPPIVWKIEGLKAVLPCTTGNPKPSVMIKGDSPLEKNSRIAVLESGSLRIHNV 180
DB 121 PKTRPPIVWKIEGLKAVLPCTTGNPKPSVMIKGDSPLEKNSRIAVLESGSLRIHNV 180
OY 181 OKEDAGQYRCVAKNSLGTATSKVYKLEFEVFAILRAPESHNTFGSFVTLHCTATGIPV 240
DB 181 OKEDAGQYRCVAKNSLGTATSKVYKLEFEVFAILRAPESHNTFGSFVTLHCTATGIPV 240
OY 241 PTTIWIENGNAVSSGSIQESVDRVIDSRLOLFTKPGITCJATNKHGKSTAKAAAT 300
DB 241 PTTIWIENGNAVSSGSIQESVDRVIDSRLOLFTKPGITCJATNKHGKSTAKAAAT 300
OY 301 ISTIAEMSKPOKNGKGYCAQYRGECVNAVYAKDALVFLNTSYADPEAOELVHTANMELK 360
DB 301 ISTIAEMSKPOKNGKGYCAQYRGECVNAVYAKDALVFLNTSYADPEAOELVHTANMELK 360
OY 361 VVSPVCRPAEALLCNHIIFQECSPGVVPTPIPCREYCAVAVELFCAKEMLVNEEKTHTG 420
DB 361 VVSPVCRPAEALLCNHIIFQECSPGVVPTPIPCREYCAVAVELFCAKEMLVNEEKTHTG 420
OY 421 LVYRSEHNLISVPCSKLPSMMDPTACARLPDLNKNENKTPPTMTSKPSVDINLPS 480
DB 421 LVYRSEHNLISVPCSKLPSMMDPTACARLPDLNKNENKTPPTMTSKPSVDINLPS 480
OY 481 SSSSSSVSPPTYSMTVITISMSFAFVLTTTLTYCCRRRQWKNKKRESAAVTLTTP 540
DB 481 SSSSSSVSPPTYSMTVITISMSFAFVLTTTLTYCCRRRQWKNKKRESAAVTLTTP 540
OY 541 SELLDRLHPNPKYQRMPLLNKLSLEPRNNIEYVDIGSGARGVQARAPGLLY 600
DB 541 SELLDRLHPNPKYQRMPLLNKLSLEPRNNIEYVDIGSGARGVQARAPGLLY 600
OY 601 EPTTVAVKMLKEASADQADQOREALMAEPDNPNIYKLVCAVGRMCLLEFYMAV 660
DB 601 EPTTVAVKMLKEASADQADQOREALMAEPDNPNIYKLVCAVGRMCLLEFYMAV 660
OY 661 GOLNEERLMSPTVCSLSHSDLSMAQVSSPPRLSCAEOLCTARQVAAAGVYSEK 720
DB 661 GOLNEERLMSPTVCSLSHSDLSMAQVSSPPRLSCAEOLCTARQVAAAGVYSEK 720
OY 721 FVHRDLATRNCLGVENKVVKIADFGLSRIYASDYKAKENDAIPIRMHPESIIFNRYT 780
DB 721 FVHRDLATRNCLGVENKVVKIADFGLSRIYASDYKAKENDAIPIRMHPESIIFNRYT 780
OY 781 TSSDWAVYVWLEIFSYGLQPYGHAHEBVYYVDGNILSCPENCPVELYNLMRLCWS 840
DB 781 TSSDWAVYVWLEIFSYGLQPYGHAHEBVYYVDGNILSCPENCPVELYNLMRLCWS 840
OY 841 KLPADRPSTSIHRILERMCEKRAEGTVSV 869
DB 841 KLPADRPSTSIHRILERMCEKRAEGTVSV 869

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RESULT 4
AAW26506
ID AAW26506 standard: Protein: 869 AA.
AC AAW26506:
XX

06-JAN-1998 (first entry)
DE Human Dmk receptor.
XX Dmk receptor: tyrosine kinase receptor; signal transduction; assay;
XX therapy; diagnosis; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; Lou Gehrig's disease;
XX idiopathic torsion dystonia; muscle atrophy.
OS Homo sapiens.
XX
XX US5656473-A.
XX
XX 12-AUG-1997.
PD

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XX 21-JUL-1993; 93US-0095658.
PF 19-JAN-1995; 95US-0374834.
XX 21-JUL-1993; 93US-0095658.
PR (REG-) REGENERON PHARM INC.
XX Rojas EA, Valenzuela DM;
XX WPI: 1997-414593/38.
DR N-PSDB: AAT87073.
XX New isolated human denervated muscle kinase receptor - used to
PT develop products for the diagnosis and treatment of neurological,
PT muscle or neuromuscular disorders
PS Claim 4; Column 31-36; 31pp; English.
XX This polypeptide comprises the human Dmk receptor (AAW26506), a novel
CC tyrosine kinase receptor that is expressed in high levels in
CC denervated muscle. Its amino acid sequence was deduced from an
CC isolated nucleic acid molecule (see AAT87073). The Dmk receptor can
CC be used to screen for agents that interact with Dmk. Agents that
CC bind to the receptor may mediate survival and differentiation in
CC cells naturally expressing the receptor, but may also confer survival
CC and proliferation when used to treat cells engineered to express the
CC receptor. Dmk receptor polypeptides and polynucleotides can also be
CC used for detecting aberrancies in the function or expression of the
CC receptor which may be used in the diagnosis of muscular or other
CC disorders. Manipulation of the receptor or agonists which bind this
CC receptor may be used to treat neurological diseases, diseases of
CC muscle or neuromuscular unit disorders, including Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis (Lou
CC Gehrig's disease), idiopathic torsion dystonia and muscle atrophy.
CC The extracellular domain (ECD) of the receptor can be used to block
CC the binding of receptor to target cells. A receptorbody comprising
CC the ECD fused to a human Ig gamma-1 constant region is claimed.
SO Sequence 869 AA;

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Query Match 99.8%; Score 4558; DB 18; Length 869;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MELVNIPIVHLITLVAFSGTEKLPKAPVITPTPLTYVALVEVATFMKAVSYQPEIS 60
DB 1 MELVNIPIVHLITLVAFSGTEKLPKAPVITPTPLTYVALVEVATFMKAVSYQPEIS 60
OY 61 WTRNKLILKLPDTRYSIKRENGCOLLITLSYEDSDGDIYCCCTANNGVGAIVESGALOVKAK 120
DB 61 WTRNKLILKLPDTRYSIKRENGCOLLITLSYEDSDGDIYCCCTANNGVGAIVESGALOVKAK 120
OY 61 WTRNKLILKLPDTRYSIKRENGCOLLITLSYEDSDGDIYCCCTANNGVGAIVESGALOVKAK 120
DB 61 WTRNKLILKLPDTRYSIKRENGCOLLITLSYEDSDGDIYCCCTANNGVGAIVESGALOVKAK 120
OY 121 PKTRPPIVWKIEGLKAVLPCTTGNPKPSVMIKGDSPLEKNSRIAVLESGSLRIHNV 180
DB 121 PKTRPPIVWKIEGLKAVLPCTTGNPKPSVMIKGDSPLEKNSRIAVLESGSLRIHNV 180
OY 181 OKEDAGQYRCVAKNSLGTATSKVYKLEFEVFAILRAPESHNTFGSFVTLHCTATGIPV 240
DB 181 OKEDAGQYRCVAKNSLGTATSKVYKLEFEVFAILRAPESHNTFGSFVTLHCTATGIPV 240
OY 241 PTTIWIENGNAVSSGSIQESVDRVIDSRLOLFTKPGITCJATNKHGKSTAKAAAT 300
DB 241 PTTIWIENGNAVSSGSIQESVDRVIDSRLOLFTKPGITCJATNKHGKSTAKAAAT 300
OY 301 ISTIAEMSKPOKNGKGYCAQYRGECVNAVYAKDALVFLNTSYADPEAOELVHTANMELK 360
DB 301 ISTIAEMSKPOKNGKGYCAQYRGECVNAVYAKDALVFLNTSYADPEAOELVHTANMELK 360
OY 361 VVSPVCRPAEALLCNHIIFQECSPGVVPTPIPCREYCAVAVELFCAKEMLVNEEKTHTG 420
DB 361 VVSPVCRPAEALLCNHIIFQECSPGVVPTPIPCREYCAVAVELFCAKEMLVNEEKTHTG 420

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OY 421 LYSEHLLSVKCSKLPKSHMDPTACARLPHLDYKNENLKEPPMTSSKPSVDINPLPS 480
XX |||||
DB 421 lysemhllsvpecsklpshmdptacarlphldynkenlktprmtsskpsvdinpls 480
OY 481 SSSSFVSPTYSMTVIISMSFAIFVLLITTLVCCRKKRWKKNKRESAAVTLTLP 540
XX |||||
DB 481 ssssfvsptysmtviiismssfaifvllittllyccrrkkqwnkkresaaavtltlp 540
OY 541 SELLDRLHPNMYQRMPLLNPKLLEPRNNIEYVDIGGAGRVFOARAPGLPY 600
XX |||||
DB 541 sellldrlhpnmqrmpllnpkllsleprnnieyvdigagatgrvfgarapglpy 600
OY 601 EPTMVAVKMLKEESADMDQADFOREALMAEFNDPNIVKLLGVCAGKPMCLIFEYMA 660
XX |||||
DB 601 eptmvaavkmlkeesaadmdqadfgreaalmaefndpnivkllgvcavgkpmcllfeymay 660
OY 661 GDLNERTSMSPHTVCSLSHSDLSMAQVSSPEPPPLSCADJCLARQVAAAGVYSEK 720
XX |||||
DB 661 gdlneertsmshpvtcslsbsdlsmaqvspppplscaeqclclargvaagmayiserk 720
OY 721 FVHRDLATRNCLVGENMVKIADFGLSRNIYSADYKKNENDAPIRMMPESEIENRYT 780
XX |||||
DB 721 fvhrdlatrnclvgenmvvkiafdglsrniysadykkanendaiprtmpsesifeyryt 780
OY 781 TESDVAVYVIMETIFSTCLQPYGMAHEVITYVRDGNILSCPENCPELYNLMLCWS 840
XX |||||
DB 781 tesdvavayvimeifstclqpyygmaheviyyvrdsnllscpenccpelynlmlcws 840
OY 841 KLPADRPSTSIHRIERMCERAEQTVSV 869
XX |||||
DB 841 klpadrpstsihriermceraeqtvsv 869

RESULT 5
AAM26610
ID AAM26610 standard; Protein: 868 AA.
AC AAM26610;
XX
DT 27-JAN-1998 (first entry)
XX
DE Rat muscle-specific kinase (Musk).
XX
KW Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; rat;
KW ligand; agrin; diagnosis; therapy.
XX
OS Rattus sp.
XX
FH Key location/Qualifiers
FT Peptide 1..19
FT /Label- S1g-peptide
FT Domain 21..492
FT /Label- Extracellular_domain
FT Domain 493..521
FT /Label- Transmembrane_domain
FT Domain 522..868
FT /Label- Intracellular_domain
XX
PN W09721811-A2.
XX
PD 19-JUN-1997.
XX
PE 13-DEC-1996; 96WO-US20696.
XX
PR 10-MAY-1996; 96US-0644271.
PR 15-DEC-1995; 95US-0008657.
XX
PA (REGC-) REGENERON PHARM INC.
XX
PI Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;
XX
DR WPI: 1997-332783/30.

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DR N-PSDB: AAT90472.
XX
PT Nucleotide sequences encoding human agrin and muscle specific kinase
PT and related receptor - used in diagnosis and treatment of disorder
PT with muscle atrophy
XX
PS Example 1; Fig 1; 120pp; English.
XX
CC This polypeptide comprise a novel rat receptor tyrosine kinase
CC designated muscle specific kinase (Musk) that is expressed in
CC normal and denervated muscle. Musk is alternatively referred to
CC Dmk for denervated muscle kinase. The amino acid sequence was
CC deduced from an isolated cDNA clone (see AAT90472). Human Musk (see
CC AAM26611) has also been identified. Use of Musk to generate anti-
CC Musk antibodies and in the diagnosis of neurological or other
CC disorders is disclosed. Assay systems that may be used to detect
CC and/or measure ligands that bind the musk gene product are provided.
CC A claimed method of promoting the growth, differentiation or
CC survival of Musk receptor-expressing cells involves administration
CC to the cell of agrin (see AAM26605). Such cells include muscle,
CC heart, spleen, ovary and retina cells, or cells genetically
CC engineered to express the Musk receptor.
XX
SQ Sequence 868 AA;
OY
Query Match 93.9%; Score 4292.5; DB 18; Length 868;
Beat Local Similarity 93.2%; Fred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;
OY 1 MRELVINPLVHILTLVAESGTEKLPKAPYITPLETVDAIVEVATFMCVAVESYPOPEIS 60
DB 1 mrelvniplqlmlltvalsfsteklpkapyitpletvdaivevatfmcavasyppels 60
OY 61 WTRNKKILKLPTRKYSIRENGQLITLTVESDSDGIYCCCTANNVGGAVESGALQVKK 120
DB 61 wtrnkilkllptryksirengqlitltsvedsdgilycctannvggavescgalqvkk 120
OY 121 PKITRPINVKIIEGLKAVLPCTTGNRPSPSWIKGDSPLRENSRIANVLESGSLRIHV 180
DB 121 pkitrrpinvkiieglkavlpcttgnrpspswikgdsplrensriavlesgslrlhiv 180
OY 181 OKEDAGQYRCVAKNSLGTATYSKVVKLEFEVFAIRLIRAPESHNVTFGSEFTLLCTRTGIPV 240
DB 181 okedagqyrcvaknslgtatyskvvklfevfarlirapeshnvtfgstfllctctgipv 240
OY 241 PRTIENGNAVSSGSIDESVAKDRYIDSRLOLFTKPGLYCIATNKGKFSKAAAT 300
DB 241 prtienngnavssgsidesvakdryidsrlofltkpglyciatnkgkfstakaaat 300
OY 301 ISIAEMSKPQKDNKGYCAQYRGECNAVLAKDALVFINTSYADPREAQELVHTAMNEX 360
DB 301 isiaemskpqkdnkgycaoyrgecnavlakdalvfintsyadpreaqelvyhtamnelx 360
OY 361 VSIAEWSKSGKESKYCGYRGVCDVAVKDSLVFINTSYDPEAEGLIHTAMNEX 360
DB 361 vsiaewsksgkeskygcgyrgvcdavavkdslvfintsydpaeagellhtamnelx 360
OY 421 VVSPVCRPAEALLCNHIFQECSPGVPTPIPICREYCLAVKELPCANEMVMEKTRHG 420
DB 421 vvspvcrpaeeallcnhlfqecspgvptpipticreyclavkelpcanemvmeektrhg 420
OY 481 LYSEHLLSVKCSKLPKSHMDPTACARLPHLDYKNENLKEPPMTSSKPSVDINPLPS 480
DB 481 lysemhllsvpecsklpshmdptacarlphldynkenlktprmtsskpsvdinpls 480
OY 541 SELLDRLHPNMYQRMPLLNPKLLEPRNNIEYVDIGGAGRVFOARAPGLPY 600
DB 541 sellldrlhpnmqrmpllnpkllsleprnnieyvdigagatgrvfgarapglpy 600
OY 601 EPTMVAVKMLKEESADMDQADFOREALMAEFNDPNIVKLLGVCAGKPMCLIFEYMA 660
DB 601 eptmvaavkmlkeesaadmdqadfgreaalmaefndpnivkllgvcavgkpmcllfeymay 660

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QY 661 GDINEFLRSMSPHTVCSLSHSDLSMRAQVSSPPPELSCAEOLCIARQVAGMAYLSERK 720
Db 660 gdineflrsmshphtvcslshsdlsstrarvssppplscaeqlclarqvaagmaylserk 719
QY 721 FVHRDLATRNCLVGENNVKVIADFGLSRNTYSADYKKAENDAIPIRKMPPESTIFYNRYT 780
Db 720 fvhrrdlatrncclvgenmvvkiadfglsrntysadykkadgndaiplrmppestifynryt 779
QY 781 TESDVAVAGVVLMEIFSXYGLQPIYGGMAHEEVIYYVDGNILSCPEKCPVELYNLMRLCMS 840
Db 780 tesdvavagvvlmeifsyglqpiyggmaheevlyyvrtdgnllscpenclplynmlrlcms 839
QY 841 KLPADRPSTSHIRLERMRCERAEGETVSV 869
Db 840 klpadrpstshirllqrmcerageltgyv 868

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RESULT 6

AAW26507

ID AAW26507 standard; Protein: 868 AA.

AC AAW26507;

D1 06-JAN-1998 (first entry)

DE Rat Dmk receptor.

KM Dmk receptor; tyrosine kinase receptor; signal transduction; assay;
 KW therapy; diagnosis.
 OS Rattus sp.

FT Key Location/Qualifiers
 FT Peptide 1..19
 FT Domain /Label- Sig-peptide
 FT Domain /Label- Extracellular
 FT Domain /Label- Transmembrane
 FT Domain /Label- Intracellular

D55656473-A.

12-AUG-1997.

21-JUL-1993; 93US-0095658.

19-JAN-1995; 95US-0374834.

21-JUL-1993; 93US-0095658.

(REGG-) REGENERON PHARM INC.

Rojas EA, Valenzuela DM;

WPI: 1997-414593/38.

N-PSDB: AAT87074.

PT New isolated human denervated muscle kinase receptor - used to
 develop products for the diagnosis and treatment of neurological,
 muscle or neuromuscular disorders

Example 1; Column 19-24; 31pp; English.

CC This polypeptide sequence comprises the rat Dmk receptor, a novel
 CC tyrosine kinase receptor that is expressed at high levels in
 CC denervated muscle. Its amino acid sequence was deduced from an
 CC isolated cDNA clone (see AAT87074). Human Dmk receptor (see
 CC AAW26506) has also been identified and can be used to develop
 CC products for the diagnosis and treatment of neurological, muscle
 CC or neuromuscular disorders.

SQ Sequence 868 AA:

Query Match 93.9%; Score 4292.5; DB 18; Length 868;

Best Local Similarity 93.2%; Pred. No. 0;

Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

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QY 1 MRELNIPLVHLTLVAASGTEKLPKAVITTPLETVDALEEVATPEKAVESYPOPEIS 60
Db 1 mrelniplvhlmltlvaalsgteklpkavittpletvdaaleevatepkavesypqpeis 60
QY 61 WTRNKLILKLPDTRYISIRENQLITLSEVSDDSITCYCTANNNGAVESGALQVYMK 120
Db 61 wtrnklilkldtryisirengqlitlilevsddgilycctannvvgavesgallqvymk 120
QY 121 PKITRPPIVNVKIIIEGLKAVLPCTTWGNPKPSVSWIKGDSPLRENSRIAVLESGSLRHNV 180
Db 121 pkitrppinvklliegkavlpcttmgnpkpsvswikgdsalrensrlavlesgsrlnhv 180
QY 181 QKEDAGYRCVAKNSLGRVYKLEFEVFARILRAPESHNNTFGSVTLHCTATGIPV 240
Db 181 qkedagyrvcaknslgrvylklefevfartlraperhnnntfgsvtllhctatgipv 240
QY 241 PTIWIENGNAVSSGSIQESYKDRVIDSRLOLFTTKPGLYCIATNKHGEKSTAKAAT 300
Db 241 ptlwiengnavssgsiqesykdrvidsrloqlfttkpglyciatnkhgefstakaat 300
QY 301 ISIAEKSPKQDNKGYCAQYRGEVCNAVLAQDALVFLNTSYADPEAOELLVHTAMNELK 360
Db 301 isiaekspkqdnkgycaqyrgevcnavlaqdalvflntsyadpeaellvhtamnelk 360
QY 361 VSPFCRPAEALCNHIFQCSPGVYPTPIQRECLAVKELFCRKEMLVMEKTHRG 420
Db 361 vspfcrpaeealcnhlfqcspgvypptpiqreclavkelfcrkemlvmekthrg 420
QY 421 LYREBMLLSVPCSKLPSMHMDPTACARLPHLDYKNEKLTPEPMTSKPSVDIPNLS 480
Db 421 lyrebmlslsvpcsklpsmhmdptacarlphtdyknektlpepmtskpsvdipnlps 480
QY 481 SSSSFVSPTSMVTYIISTMSFAIVLITITLYCCRRKKOKKKKRESAAVTLTLP 540
Db 481 ssssfvsptsmvtiyiistmsfaivlittitlyccrrkkokkkkresaaavtltlp 540
QY 541 SELLDRLHPNPYQRMPLLNPKLSLEYPRNIEYVRDIEGAFGRVQARAGILPY 600
Db 540 selldrlhpnpyqrmpllnpkllsleyprnieyvrldiegafgrvqaragilpy 600
QY 601 EPTIMVAVKMLKEBASADQADFOREALMAEDNPNIIVKLGCAVAGKPMCLFEYMAV 660
Db 600 eptimvavkmlkebasadqadfgreaalmafndpniivkllgycavagkpmclfeymav 659
QY 661 GDINEFLRSMSPHTVCSLSHSDLSMRAQVSSPPPELSCAEOLCIARQVAGMAYLSERK 720
Db 660 gdineflrsmshphtvcslshsdlsstrarvssppplscaeqlclarqvaagmaylserk 719
QY 721 FVHRDLATRNCLVGENNVKVIADFGLSRNTYSADYKKAENDAIPIRKMPPESTIFYNRYT 780
Db 720 fvhrrdlatrncclvgenmvvkiadfglsrntysadykkadgndaiplrmppestifynryt 779
QY 781 TESDVAVAGVVLMEIFSXYGLQPIYGGMAHEEVIYYVDGNILSCPEKCPVELYNLMRLCMS 840
Db 780 tesdvavagvvlmeifsyglqpiyggmaheevlyyvrtdgnllscpenclplynmlrlcms 839
QY 841 KLPADRPSTSHIRLERMRCERAEGETVSV 869
Db 840 klpadrpstshirllqrmcerageltgyv 868

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RESULT 7

AAW2717

ID AAW2717 standard; Protein: 868 AA.

AC AAW2717;

